

263365us-seq-list-082310 (2).txt
SEQUENCE LISTING

<110> weill, Mylene
Fort, Philippe
Raymond, Michel
Pasteur, Nicole

<120> NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF

<130> 263365US0XPCT

<140> 10/518,072

<141> 2004-12-16

<150> FR 02/07622

<151> 2002-06-20

<150> FR 02/13799

<151> 2002-11-05

<160> 150

<170> PatentIn version 2.1

<210> 1

<211> 524

<212> PRT

<213> Anopheles gambiae

<400> 1

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Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn Ser
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Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
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Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
      85          90          95
Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
      100          105          110
Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
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Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
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 180 185 190
 Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu Leu
 195 200 205
 Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr Leu
 225 230 235 240
 Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro Ser
 245 250 255
 Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His Val
 260 265 270
 Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro Phe
 275 280 285
 Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg Ser
 290 295 300
 Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser Asn
 305 310 315 320
 Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu Leu
 325 330 335
 Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln Ala
 340 345 350
 Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala Ile
 355 360 365
 Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser Asn
 370 375 380
 Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys Asn
 385 390 395 400
 Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val Tyr
 405 410 415
 Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg Trp
 420 425 430
 Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu Pro
 435 440 445
 Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser Arg
 450 455 460
 Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro Asn
 465 470 475 480
 Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr Ala
 485 490 495

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 <212> DNA
 <213> Anopheles gambiae

<220>
 <221> CDS
 <222> (1)..(1932)

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 aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc 96
 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser 30
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 gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144
 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser 45
 35 40
 gga gca acg ccg cgg cga cgc ggc ctg acg agg cgc gag tca aac tcg 192
 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser 60
 50 55
 gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240
 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg 80
 65 70
 atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288
 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val 95
 85 90
 tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg cta cgg ttc 336
 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe 110
 100 105
 cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc 384
 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr 125
 115 120
 aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac 432
 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp 140
 130 135
 ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac 480
 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp 160
 145 150 155
 tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg 528
 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala 175
 165 170
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 180 185

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ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac	Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn	225	230	235	720
ctt gcg cta cgc tgg gtg cgg gac aac att cac cgg ttc ggt ggc gat	Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp	245	250	255	768
ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg	Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val	260	265	270	816
tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag cgg gcc	Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala	275	280	285	864
atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc	Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg	290	295	300	912
gag gaa gcc aca cta aga gca ctg cgg ttg gcc gag gcg gtc ggc tgc	Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys	305	310	315	960
ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc	Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly	325	330	335	1008
aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att	Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile	340	345	350	1056
tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag	Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu	355	360	365	1104
acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc	Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile	370	375	380	1152
ctc acc ggc agc aac acg gag gag ggc tac tac ttc atc atc tac tac	Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr	385	390	395	1200
ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag	Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu	405	410	415	1248
gag ttc ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg	Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala	420	425	430	1296

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aac ccg aac agc aac cgg gac gcg ctg gac aag atg gtg ggc gac tat Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr 450 455 460	1392
cac ttc acc tgc aac gtg aac gag ttc gcg cag ccg tac gcc gag gag His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu 465 470 475 480	1440
ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn 485 490 495	1488
ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr 500 505 510	1536
gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu 515 520 525	1584
aaa gac ttt agc cgg aag atc atg cga tac tgg tcc aac ttt gcc aaa Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys 530 535 540	1632
acc ggg aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp 545 550 555 560	1680
ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn 565 570 575	1728
acg tcc ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp 580 585 590	1776
aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly 595 600 605	1824
cca gca ccg cct agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg 610 615 620	1872
cct gat ctg atc gtg ctg ctg gtg tcg ctg ctt acg gcg acc gtc aga Pro Asp Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg 625 630 635 640	1920
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Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
 35      40      45
Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
 50      55      60
Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
 65      70      75      80
Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
 85      90      95
Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
100      105      110
Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
115      120      125
Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
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Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
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Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala
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Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala
180      185      190
Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val
195      200      205
Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe
210      215      220
Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn
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Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp
245      250      255
Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val
260      265      270
Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala
275      280      285
Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg
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Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys
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Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly
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 370 375 380
 Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr
 385 390 395 400
 Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu
 405 410 415
 Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala
 420 425 430
 Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp
 435 440 445
 Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr
 450 455 460
 His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu
 465 470 475 480
 Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn
 485 490 495
 Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr
 500 505 510
 Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu
 515 520 525
 Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys
 530 535 540
 Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp
 545 550 555 560
 Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn
 565 570 575
 Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp
 580 585 590
 Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly
 595 600 605
 Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg
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 Phe Ile Gln

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 <212> DNA
 <213> Anopheles gambiae strain KISUMU

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 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
 20 25 30
 gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144
 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
 35 40 45
 gga gca acg ccg cgg cga cgc ggt ctg acg agg cgc gag tcc aac tcg 192
 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
 50 55 60
 gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240
 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
 65 70 75 80
 atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288
 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
 85 90 95
 tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg tta cgg ttc 336
 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
 100 105 110
 cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc 384
 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
 115 120 125
 aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac 432
 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
 130 135 140
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 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
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 180 185 190
 acc ctg gac gtg tac gac cac cgg gcg ctt gcg tcg gag gag aac gtg 624
 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val
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 atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt 672

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225				230					235								
ctt	gcg	cta	cgc	tgg	gtg	cgg	gac	aac	att	cac	cgg	ttc	ggt	ggt	gat	768	
Leu	Ala	Leu	Arg	Trp	Val	Arg	Asp	Asn	Ile	His	Arg	Phe	Gly	Gly	Asp	255	
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Pro	Ser	Arg	Val	Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Val	Ser	Val	260	
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tcg	ctg	cat	ctg	ctg	tcc	gcc	ctg	tcc	cgc	gat	ctg	ttc	cag	cgg	gcc	864	
Ser	Leu	His	Leu	Leu	Ser	Ala	Leu	Ser	Arg	Asp	Leu	Phe	Gln	Arg	Ala	275	
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atc	ctg	cag	agc	ggc	tcg	ccg	acg	gca	ccg	tgg	gca	ttg	gta	tcg	cgc	912	
Ile	Leu	Gln	Ser	Gly	Ser	Pro	Thr	Ala	Pro	Trp	Ala	Leu	Val	Ser	Arg	290	
	290					295					300						
gag	gaa	gcc	acg	cta	aga	gca	ctg	cgg	ttg	gcc	gag	gcg	gtc	ggc	tgc	960	
Glu	Glu	Ala	Thr	Leu	Arg	Ala	Leu	Arg	Leu	Ala	Glu	Ala	Val	Gly	Cys	305	
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ccg	cac	gaa	ccg	agc	aag	ctg	agc	gat	gcg	gtc	gag	tgt	ctg	cgc	ggc	1008	
Pro	His	Glu	Pro	Ser	Lys	Leu	Ser	Asp	Ala	Val	Glu	Cys	Leu	Arg	Gly	325	
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aag	gat	ccg	cac	gtg	ctg	gtc	aac	aac	gag	tgg	ggc	acg	ctc	ggc	att	1056	
Lys	Asp	Pro	His	Val	Leu	Val	Asn	Asn	Glu	Trp	Gly	Thr	Leu	Gly	Ile	340	
			340					345					350				
tgc	gag	ttc	ccg	ttc	gtg	ccg	gtg	gtc	gac	ggt	gcg	ttc	ctg	gac	gag	1104	
Cys	Glu	Phe	Pro	Phe	Val	Pro	Val	Val	Asp	Gly	Ala	Phe	Leu	Asp	Glu	355	
		355				360						365					
acg	ccg	cag	cgt	tcg	ctc	gcc	agc	ggg	cgc	ttc	aag	aag	acg	gag	atc	1152	
Thr	Pro	Gln	Arg	Ser	Leu	Ala	Ser	Gly	Arg	Phe	Lys	Lys	Thr	Glu	Ile	370	
						375					380						
ctc	acc	ggc	agc	aac	acg	gag	gag	ggc	tac	tac	ttc	atc	atc	tac	tac	1200	
Leu	Thr	Gly	Ser	Asn	Thr	Glu	Glu	Gly	Tyr	Tyr	Phe	Ile	Ile	Tyr	Tyr	385	
				390					395					400			
ctg	acc	gag	ctg	ctg	cgc	aag	gag	gag	ggc	gtg	acc	gtg	acg	cgc	gag	1248	
Leu	Thr	Glu	Leu	Leu	Arg	Lys	Glu	Glu	Gly	Val	Thr	Val	Thr	Arg	Glu	405	
				405					410					415			
gag	ttc	ctg	cag	gcg	gtg	cgc	gag	ctc	aac	ccg	tac	gtg	aac	ggg	gcg	1296	
Glu	Phe	Leu	Gln	Ala	Val	Arg	Glu	Leu	Asn	Pro	Tyr	Val	Asn	Gly	Ala	420	
			420					425					430				
gcc	cgg	cag	gcg	atc	gtg	ttc	gag	tac	acc	gac	tgg	acc	gag	ccg	gac	1344	
Ala	Arg	Gln	Ala	Ile	Val	Phe	Glu	Tyr	Thr	Asp	Trp	Thr	Glu	Pro	Asp	435	
			435				440					445					
aac	ccg	aac	agc	aac	cgg	gac	gcg	ctg	gac	aag	atg	gtg	ggc	gac	tat	1392	
Asn	Pro	Asn	Ser	Asn	Arg	Asp	Ala	Leu	Asp	Lys	Met	Val	Gly	Asp	Tyr	450	
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ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac	1488
Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn	
485 490 495	
ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac	1536
Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr	
500 505 510	
gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag	1584
Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu	
515 520 525	
aaa gac ttt agc cgg aag atc atg cga tac tgg tct aac ttt gcc aaa	1632
Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys	
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Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp	
545 550 555 560	
ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac	1728
Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn	
565 570 575	
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Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp	
580 585 590	
aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg	1824
Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly	
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Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg	
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<211> 643

<212> PRT

<213> Anopheles gambiae strain KISUMU

<400> 5

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25

30

Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser

35

40

45

263365us-seq-list-082310 (2).txt

Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
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Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
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Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
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Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
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Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
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Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala
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Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala
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225 230 235 240
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Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys
305 310 315 320
Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly
325 330 335
Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile
340 345 350
Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu
355 360 365
Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile
370 375 380

263365us-seq-list-082310 (2).txt

Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr
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Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp
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Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr
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His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu
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Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn
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Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr
500 505 510

Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu
515 520 525

Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys
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Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp
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Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn
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Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp
580 585 590

Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly
595 600 605

Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg
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Phe Ile Gln

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<212> DNA

<213> Culex pipiens strain S-LAB

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263365us-seq-list-082310 (2).txt

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263365us-seq-list-082310 (2).txt

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50 55 60
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85 90 95
Asp Ala Glu Leu Gly Thr Leu Glu Arg Glu His Ile His ser Thr Thr
100 105 110
Thr Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Ser Ser Asp Ala Thr
115 120 125
Asp Ser Asp Pro Leu Val Ile Thr Thr Asp Lys Gly Lys Ile Arg Gly
130 135 140
Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly
145 150 155 160
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Arg Pro Ala Glu Arg Trp Thr Gly val Leu Asn Ala Thr Lys Pro Pro
180 185 190
Asn Ser Cys val Gln Ile val Asp Thr val Phe Gly Asp Phe Pro Gly
195 200 205
Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr
210 215 220
Ile Asn Val val val Pro Arg Pro Arg Pro Lys Asn Ala Ala val Met
225 230 235 240
Leu Trp Ile Phe Gly Gly Gly Phe Tyr ser Gly Thr Ala Thr Leu Asp
245 250 255
val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn val Ile val val
260 265 270
Ser Leu Gln Tyr Arg val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr
275 280 285
Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu
290 295 300
Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg
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263365us-seq-list-082310 (2).txt

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Ala Thr Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Thr Lys Asp Pro
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Asn Glu Leu Val Asp Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe
405 410 415

Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln
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Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Asp Ile Leu Thr Gly
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Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu
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Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu
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Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln
485 490 495

Ala Ile Val Phe Glu Tyr Thr Asp Trp Ile Glu Pro Asp Asn Pro Asn
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Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr
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Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn
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Val Phe Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro
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Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly
565 570 575

Glu Pro Leu Asn Ser Ala Leu Gly Tyr Gln Asp Asp Glu Lys Asp Phe
580 585 590

Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn
595 600 605

Pro Asn Pro Ser Thr Pro Ser Val Asp Leu Pro Glu Trp Pro Lys His
610 615 620

Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Thr Phe
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Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Ser Ala Leu Gly Tyr
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 <213> Aedes aegypti

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Ser Asp Leu Gly Tyr
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 <213> Aedes albopictus

<400> 10

263365us-seq-list-082310 (2).txt

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 65 70 75 80
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60

263365us-seq-list-082310 (2).txt

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 85 90

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<400> 14
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
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263365us-seq-list-082310 (2).txt

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35 40 45

Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
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35 40 45

Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
50 55 60

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<213> Anopheles pseudopunctipennis

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263365us-seq-list-082310 (2).txt

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 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 <212> PRT
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 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
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 85 90

263365us-seq-list-082310 (2).txt

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 85 90

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 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 Page 21

263365us-seq-list-082310 (2).txt

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263365us-seq-list-082310 (2).txt

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<210> 23
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<212> DNA
<213> Anopheles gambiae strain KISUMU

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<211> 273
<212> DNA
<213> Culex pipiens strain S-LAB

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caggacgacg agaaggactt tagccggaag att 273

<210> 25
<211> 273
<212> DNA
<213> Culex pipiens strain SR

<400> 25
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<210> 26
<211> 273
<212> DNA
<213> Aedes aegypti

<400> 26
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tacatgtatc tgtacactca tagaagcaaa ggtaaccctt ggccacgggtg gaccgggtgtg 180
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<210> 27
<211> 273
<212> DNA
<213> Aedes albopictus

<400> 27
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<210> 28
<211> 273
<212> DNA
<213> Anopheles darlingi

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<210> 29
<211> 273

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<212> DNA

<213> Anopheles sunaicus

<400> 29

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accgaggacg agaaggaactt tagccggaag atc 273
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<210> 30

<211> 273

<212> DNA

<213> Anopheles minimus

<400> 30

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accgaagacg agaaagactt tagccggaag atc 273
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<210> 31

<211> 273

<212> DNA

<213> Anopheles moucheti

<400> 31

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tacatgtacc tgtacacgca ccgaagcaaa ggcaacccgt ggccacgctg gaccggcggtt 180
atgcacgggtg acgagattaa ctacgtgttc ggggaaccgc tcaacccaag cctcggctac 240
accgaagacg agaaagactt tagccggaag atc 273
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<210> 32

<211> 273

<212> DNA

<213> Anopheles arabiensis

<400> 32

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accgaggacg agaaagactt tagccggaag atc 273
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<210> 33

<211> 273

<212> DNA

<213> Anopheles funestus

<400> 33

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accgaggacg agaaagactt tagccggaag atc 273
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<210> 34
<211> 273
<212> DNA
<213> *Anopheles pseudopunctipennis*

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accgaggacg agaaggactt tagccgcaag atc 273

<210> 35
<211> 273
<212> DNA
<213> *Anopheles sacharovi*

<400> 35
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<210> 36
<211> 273
<212> DNA
<213> *Anopheles stephensi*

<400> 36
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<210> 37
<211> 273
<212> DNA
<213> *Anopheles albimanus*

<400> 37
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accgacgacg agaagggttt cagccggaag atc 273

<210> 38
<211> 273
<212> DNA
<213> *Anopheles nili*

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<210> 39
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 39
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24

<210> 40
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 40
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24

<210> 41
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<220>
 <223> Synthetic DNA

<400> 41
 ggygckacma tgtggaaycc

20

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 <211> 24
 <212> DNA
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<220>
 <223> Synthetic DNA

<400> 42
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24

<210> 43
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<220>
 <223> Synthetic DNA

<400> 43
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<400> 44
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<210> 45
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<220>
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<400> 45
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<210> 46
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<220>
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<400> 46
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<210> 48
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<220>
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<400> 48
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<210> 49
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<223> Synthetic DNA

<400> 49

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<210> 50

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<212> DNA

<213> Artificial Sequence

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<210> 51

<211> 585

<212> PRT

<213> *Ciona intestinalis*

<400> 51

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Gly	Arg	Tyr	Leu	Ala	Ala	Gln	Gly	Gly	Val	Val	Val	Val	Ser	Ile	Asn
	130					135					140				

Tyr	Arg	Leu	Gly	Pro	Leu	Gly	Phe	Leu	Ala	Pro	Leu	Ala	Gly	Thr	Pro
145					150					155				160	

Gly	Asn	Ala	Gly	Leu	Leu	Asp	Gln	Gln	Leu	Ala	Leu	Lys	Trp	Val	Arg
			165					170						175	

Asp	Asn	Ile	Arg	Ala	Phe	Gly	Gly	Asn	Pro	Asp	Asn	Val	Thr	Leu	Met
		180						185					190		

Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Ile	Gly	Leu	His	Thr	Val	Ala	Pro

195

200

205

Ser Ser Arg Gly Leu Phe Asn Arg Val Ile Phe Gln Ser Gly Asn Gln
 210 215 220
 Met Thr Pro Trp Ser Thr Ile Ser Leu Pro Thr Ser Leu Asn Arg Thr
 225 230 235 240
 Arg Ile Leu Ala Ala Asn Leu Arg Cys Pro Asn Pro Arg Thr Ser Ser
 245 250 255
 Glu Leu Asp Val Leu Thr Cys Leu Arg Ser His Ser Ala Val Asp Val
 260 265 270
 Phe Ser Asn Ser Trp Ile Thr Gln Glu Ile Phe Asp Phe Pro Phe Val
 275 280 285
 Pro Val His Gly Thr Ser Phe Leu Pro Glu His Pro His Glu Val Thr
 290 295 300
 Arg Lys Gly Glu Gln Ala Asp Val Asp Val Met Ala Gly His Asn Thr
 305 310 315 320
 Asn Glu Gly Ser Tyr Phe Thr Leu Tyr Thr Val Pro Gly Phe Asn Ile
 325 330 335
 Ser Ser Gln Ser Ile Leu Ser Lys Lys Glu Tyr Ile Asp Gly Ile Ala
 340 345 350
 Leu Ser Gly Ile Lys Thr Asn Glu Leu Gly Arg Ser Gly Ala Ala Phe
 355 360 365
 Met Tyr Ala Asp Trp Glu Asn Pro Asp Asn Val Leu Gln Tyr Arg Asp
 370 375 380
 Gly Val Asn Glu Ile Val Gly Asp Phe His Val Val Cys Pro Thr Val
 385 390 395 400
 Leu Leu Thr Lys Arg His Ser Arg Thr Phe Ser Asn Asn Asn Val Tyr
 405 410 415
 Leu Tyr His Leu Ser Tyr Arg Leu Ser Asn Asn Pro Trp Pro Ala Trp
 420 425 430
 Met Gly Val Met His Gly Tyr Glu Ile Glu Leu Met Phe Gly Thr Pro
 435 440 445
 Trp Phe Gly Thr Ser Gln Phe Thr Ser Gly Tyr Asn Asp Val Asp Arg
 450 455 460
 Ser Val Ser Arg Arg Met Val His Tyr Trp Thr Asn Phe Ala Lys Phe
 465 470 475 480
 Gly Asn Pro Asn Gly Leu Arg Ser Ala Asn Glu Leu Asp Leu Arg Ser
 485 490 495
 Thr Asp Trp Pro Arg Phe Asp Asp Val Arg Gln Arg Tyr Leu Glu Ile
 500 505 510
 Gly Ile Asp Asp Asp Val Met Gly Pro Phe Pro Asn Ser Phe Arg Cys
 515 520 525
 Ala Phe Trp Glu Arg Tyr Leu Pro Ser Leu Lys Leu Ala Ser Ser Ala

530

Asp Met Asp Glu Val Glu Thr Lys Trp Lys Ile Glu Phe Asn Arg Trp
545 550 555 560
Thr Glu Ser Met Asp Leu Trp Asp Arg Ser Phe Lys Ala Tyr Ser Lys
565 570 575
Asp Gly Lys Gln Ser Ser Cys Pro Asn
580 585

<210> 52
<211> 583
<212> PRT
<213> Ciona savignyi

<400> 52
Gly Ser Ile Gln Gly Lys His Val Glu Val Thr Ala His Arg Gln Arg
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Tyr Gly Arg Val Ala Thr Phe Gln Gly Ile Pro Phe Ala Gln Pro Pro
20 25 30
Val Gly Glu Leu Arg Phe Ala Ala Pro Gln Pro Pro Leu Ser Trp Glu
35 40 45
Pro Asp Val Lys Met Thr Ser Glu Phe Gly Asn Ser Cys Ile Gln Glu
50 55 60
Asp Asp Leu Val Phe Gly Asn Phe Thr Gly Gly Ser Gln Met Trp Asn
65 70 75 80
Ser Pro Asn Ala Lys Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Thr
85 90 95
Pro Val Arg Ser Arg His Ala Glu Pro Leu Ala Val Leu Val Trp Ile
100 105 110
Tyr Gly Gly Ser Tyr Tyr Ser Gly Thr Ser Ser Leu Ala Leu Tyr Asp
115 120 125
Gly Arg Tyr Leu Ala Ala Thr Gly Gly Val Val Val Val Ser Leu Asn
130 135 140
Tyr Arg Leu Gly Pro Ile Gly Phe Leu Ala Pro Leu Ala Asp Glu Thr
145 150 155 160
Pro Gly Asn Val Gly Leu Leu Asp Gln Gln Leu Ala Leu Lys Trp Val
165 170 175
Arg Asp Asn Ile Arg Glu Phe Gly Gly Asn Pro Asn Asn Val Thr Val
180 185 190
Met Gly Glu Ser Ala Gly Ala Ala Ser Ile Gly Leu His Thr Ile Ala
195 200 205
Pro Ser Ser Arg Gly Leu Phe Ser Arg Val Ile Leu Gln Ser Gly Asn
210 215 220
Gln Met Thr Pro Trp Ser Thr Ile Ser Leu Glu Thr Ser Leu Asn Arg
225 230 235 240

263365us-seq-list-082310 (2).txt

Thr Arg Thr Leu Ala Ala Asn Leu Asn Cys Pro Lys Pro Arg Thr Ala
245 250 255
Ser Glu Ala Asp Ile Leu Ala Cys Leu Arg Thr His Thr Ala Asn Glu
260 265 270
Val Phe Ala Gly Ser Trp Ile Thr Lys Glu Ile Phe Asp Phe Pro Phe
275 280 285
Val Pro Val His Gly Thr Thr Phe Leu Pro Glu His Pro His Glu Val
290 295 300
Thr Arg Arg Gly Asp Gln Ala Glu Val Asp Val Leu Ala Gly Tyr Asn
305 310 315 320
Thr Asn Glu Gly Ser Tyr Phe Thr Ile Tyr Thr Val Pro Gly Tyr Asn
325 330 335
Ile Thr Thr Asn Ser Val Leu Asn Arg Arg Gln Tyr Leu Ala Gly Val
340 345 350
Asp Leu Ser Gly Leu Lys Thr Asn Thr Met Gly Arg Ser Ala Ala Ala
355 360 365
Phe Met Tyr Thr Asp Trp Glu Asn Leu Asp Asn Glu Leu Gln Tyr Arg
370 375 380
Asp Ala Val Asn Glu Ile Val Gly Asp Phe His Val Val Cys Pro Thr
385 390 395 400
Val Leu Val Ser Lys Arg His Ser Asn Ser Phe Pro Asn Arg Asn Val
405 410 415
Phe Leu Tyr His Leu Ser Tyr Arg Val Ser Thr Asn Pro Trp Pro Ile
420 425 430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Leu Met Phe Gly Thr
435 440 445
Pro Trp Phe Gly Asn Ser Lys Phe Thr Arg Gly Tyr Ser Asp Leu Asp
450 455 460
Arg Ser Val Ser Arg Arg Met Val Arg Tyr Trp Thr Asn Phe Ala Lys
465 470 475 480
Phe Gly Asn Pro Asn Gly Leu Arg Asn Gln Asn Gln Glu Leu Val Ser
485 490 495
Asp Trp Pro Arg Phe Asn Asp Val Thr Gln Arg Tyr Leu Glu Ile Ala
500 505 510
Asp Asp Asp Val Thr Met Ala Pro Phe Pro Asp Ser Phe Arg Cys Ala
515 520 525
Phe Trp Gln Lys Tyr Leu Pro Ser Leu Gln Leu Ala Ser Ser Asn Met
530 535 540
Asp Glu Val Glu Thr Lys Trp Lys Ile Glu Phe His Arg Trp Ser Glu
545 550 555 560
Ser Met Asp Leu Trp Asp Arg Ser Phe Lys Ala Tyr Ser Ser Asp Asp
565 570 575

Lys Gln Asn Ser Cys Pro Asn
580

<210> 53
<211> 645
<212> PRT
<213> Anopheles gambiae

<400> 53
Met Ala Ser Ala Tyr Tyr His Gln Ser Ala Val Gly Val Gly Asn Val
1 5 10 15
Leu Val Leu Leu Leu Gly Ala Thr Val Ile Cys Pro Ala Tyr Ala Ile
20 25 30
Ile Asp Arg Leu Val Val Gln Thr Ser Ser Gly Pro Ile Arg Gly Arg
35 40 45
Ser Thr Met Val Gln Gly Arg Glu Val His Val Phe Asn Gly Val Pro
50 55 60
Phe Ala Lys Pro Pro Val Asp Ser Leu Arg Phe Lys Lys Pro Val Pro
65 70 75 80
Ala Glu Pro Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro Pro Ser
85 90 95
Cys Ile Gln Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ala Gly Glu Glu
100 105 110
Met Trp Asn Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Tyr Leu Asn
115 120 125
Ile Trp Val Pro Thr Lys Thr Arg Leu Arg His Gly Arg Gly Leu Asn
130 135 140
Phe Gly Ser Asn Asp Tyr Phe Gln Asp Asp Asp Phe Gln Arg Gln
145 150 155 160
His Gln Ser Lys Gly Gly Leu Ala Met Leu Val Trp Ile Tyr Gly Gly
165 170 175
Gly Phe Met Ser Gly Thr Ser Thr Leu Asp Ile Tyr Asn Ala Glu Ile
180 185 190
Leu Ala Ala Val Gly Asn Val Ile Val Ala Ser Met Gln Tyr Arg Val
195 200 205
Gly Ala Phe Gly Phe Leu Tyr Leu Ala Pro Tyr Ile Asn Gly Tyr Glu
210 215 220
Glu Asp Ala Pro Gly Asn Met Gly Met Trp Asp Gln Ala Leu Ala Ile
225 230 235 240
Arg Trp Leu Lys Glu Asn Ala Lys Ala Phe Gly Gly Asp Pro Asp Leu
245 250 255
Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ser Ser Val Ser Leu His
260 265 270

263365us-seq-list-082310 (2).txt

Leu Leu Ser Pro Val Thr Arg Gly Leu Ser Lys Arg Gly Ile Leu Gln
 275 280
 Ser Gly Thr Leu Asn Ala Pro Trp Ser His Met Thr Ala Glu Lys Ala
 290 300
 Leu Gln Ile Ala Glu Gly Leu Ile Asp Asp Cys Asn Cys Asn Leu Thr
 305 310 315 320
 Met Leu Lys Glu Ser Pro Ser Thr Val Met Gln Cys Met Arg Asn Val
 325 330 335
 Asp Ala Lys Thr Ile Ser Val Gln Gln Trp Asn Ser Tyr Ser Gly Ile
 340 345 350
 Leu Gly Phe Pro Ser Ala Pro Thr Ile Asp Gly Val Phe Met Thr Ala
 355 360 365
 Asp Pro Met Thr Met Leu Arg Glu Ala Asn Leu Glu Gly Ile Asp Ile
 370 375 380
 Leu Val Gly Ser Asn Arg Asp Glu Gly Thr Tyr Phe Leu Leu Tyr Asp
 385 390 395 400
 Phe Ile Asp Tyr Phe Glu Lys Asp Ala Ala Thr Ser Leu Pro Arg Asp
 405 410 415
 Lys Phe Leu Glu Ile Met Asn Thr Ile Phe Asn Lys Ala Ser Glu Pro
 420 425 430
 Glu Arg Glu Ala Ile Ile Phe Gln Tyr Thr Gly Trp Glu Ser Gly Asn
 435 440 445
 Asp Gly Tyr Gln Asn Gln His Gln Val Gly Arg Ala Val Gly Asp His
 450 455 460
 Phe Phe Ile Cys Pro Thr Asn Glu Phe Ala Leu Gly Leu Thr Glu Arg
 465 470 475 480
 Gly Ala Ser Val His Tyr Tyr Tyr Phe Thr His Arg Thr Ser Thr Ser
 485 490 495
 Leu Trp Gly Glu Trp Met Gly Val Leu His Gly Asp Glu Val Glu Tyr
 500 505 510
 Ile Phe Gly Gln Pro Met Asn Ala Ser Leu Gln Tyr Arg Gln Arg Glu
 515 520 525
 Arg Asp Leu Ser Arg Arg Met Val Leu Ser Val Ser Glu Phe Ala Arg
 530 535 540
 Thr Gly Asn Pro Ala Leu Glu Gly Glu His Trp Pro Leu Tyr Thr Arg
 545 550 555 560
 Glu Asn Pro Ile Tyr Phe Ile Phe Asn Ala Glu Gly Glu Asp Asp Leu
 565 570 575
 Arg Gly Glu Lys Tyr Gly Arg Gly Pro Met Ala Thr Ser Cys Ala Phe
 580 585 590
 Trp Asn Asp Phe Leu Pro Arg Leu Arg Ala Trp Ser Val Pro Leu Lys
 595 600 605

Asp Pro Cys Lys Leu Asp Asp His Thr Ser Ile Ala Ser Thr Ala Arg
 610 615 620

Ala Ala Pro Thr Val Ala Leu Leu Ile Ala Leu Ser Leu Ala Val Ala
 625 630 635 640

Arg Leu Val Ala Ala
 645

<210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 54
 ccacacgccca gaagaaaaga 20

<210> 55
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 55
 aaaaacggga acgggaaag 19

<210> 56
 <211> 2109
 <212> DNA
 <213> Culex pipiens strain SR

<220>
 <221> CDS
 <222> (1)..(2106)

<400> 56
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 Met Glu Ile Arg Gly Leu Ile Thr Arg Leu Leu Gly Pro Cys His Leu
 1 5 10 15
 cga cat ctg ata ctg tgc agt ttg ggg ctg tac tcc atc ctc gtg cag 96
 Arg His Leu Ile Leu Cys Ser Leu Gly Leu Tyr Ser Ile Leu Val Gln
 20 25 30
 tcg gtc cat tgc cgg cat cat gac atc ggt agt tcg gtg gca cac cag 144
 Ser Val His Cys Arg His His Asp Ile Gly Ser Ser Val Ala His Gln
 35 40 45
 cta gga tcg aaa tac tca caa tca tcc tcg tta tcg tca tcc tcg caa 192
 Leu Gly Ser Lys Tyr Ser Gln Ser Ser Ser Leu Ser Ser Ser Ser Gln
 50 55 60
 tcg tca tcg tcg tta gct gaa gag gcc acg ctg aat aaa gat tca gat 240
 Ser Ser Ser Ser Leu Ala Glu Glu Ala Thr Leu Asn Lys Asp Ser Asp
 65 70 75 80

263365us-seq-list-082310 (2).txt

gca ttt ttt aca cca tat ata ggt cac gga gat tct gtt cga att gta Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Asp Ser Val Arg Ile Val 85 90 95	288
gat gcc gaa tta ggt aca tta gag cgc gag cat atc cat agc act acg Asp Ala Glu Leu Gly Thr Leu Glu Arg Glu His Ile His Ser Thr Thr 100 105 110	336
acc cgg cgg cgt ggc ctg acc cgg agg gag tcc agc tcc gat gcc acc Thr Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Ser Ser Asp Ala Thr 115 120 125	384
gac tcg gac cca ctg gta ata acg acg gac aag ggc aaa atc cgt gga Asp Ser Asp Pro Leu Val Ile Thr Thr Asp Lys Gly Lys Ile Arg Gly 130 135 140	432
acg aca ctg gaa gcg cca agt gga aag aag gtg gac gca tgg atg ggc Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly 145 150 155 160	480
att ccg tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro 165 170 175	528
cga ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa cca ccc Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro 180 185 190	576
aac tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggc Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly 195 200 205	624
gcg acc atg tgg aac ccg aac aca ccc ctc tcg gag gac tgt ctg tac Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr 210 215 220	672
atc aac gtg gtc gtg cca agg ccg agg ccc aag aat gcc gct gtc atg Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met 225 230 235 240	720
ctg tgg atc ttt ggg ggt agc ttc tac tcc ggg act gcc acg ttg gac Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp 245 250 255	768
gtg tac gat cat cgg acg ctg gcc tcg gag gag aac gtg atc gtg gtt Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val 260 265 270	816
tcg ctg cag tac cgt gtc gca agt ctt ggt ttt ctc ttc ctg ggc act Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr 275 280 285	864
ccg gag gca cct ggt aac gcg ggg ctg ttt gat caa aac ctg gca ctg Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu 290 295 300	912
aga tgg gtc cgc gac aac atc cac cgg ttc ggc ggt gac ccc tcg ccg Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg 305 310 315 320	960
gtc aca ctg ttc ggc gag agc gcc gga gcg gtc tcg gtt tcg ctg cac Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His 36	1008

263365us-seq-list-082310 (2).txt

325	330	335	
ctg ctg tcg gcg ctc tcg cgg gac ctg ttc cag cgg gcc atc ctc cag Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln 340 345 350	1056		
agt ggc tcc ccg acg gcc cca tgg gcg ctg gtt tcg cgc gaa gaa gct Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala 355 360 365	1104		
acg ctt aga gct ctt cgt ctg gcc gag gcc gtc aac tgt ccg cac gat Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Asn Cys Pro His Asp 370 375 380	1152		
gcg acc aag ctg agc gat gcc gtc gaa tgt ctg cga acc aag gat ccg Ala Thr Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Thr Lys Asp Pro 385 390 400	1200		
aac gag ctg gtc gac aat gag tgg ggc acg ctg ggg atc tgc gag ttt Asn Glu Leu Val Asp Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe 405 410 415	1248		
ccg ttc gtt ccg gtt gtg gac ggt gcc ttc ctc gat gag aca ccg cag Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln 420 425 430	1296		
cgt tcg ttg gcc agc ggt cgc ttc aag aaa acg gac atc ctg acc ggc Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Asp Ile Leu Thr Gly 435 440 445	1344		
agc aac acc gag gag ggt tac tac ttt atc att tac tat cta acc gaa Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu 450 455 460	1392		
ctg ctc agg aaa gag gaa ggg gtc acg gta aca cgc gag gag ttc cta Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu 465 470 475 480	1440		
cag gcc gtc cgg gag ttg aat ccg tac gtg aac ggt gcc gcc cgg cag Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln 485 490 495	1488		
gcc atc gtg ttc gag tac acg gac tgg atc gaa ccg gac aac ccg aac Ala Ile Val Phe Glu Tyr Thr Asp Trp Ile Glu Pro Asp Asn Pro Asn 500 505 510	1536		
agc aac cgt gac gcg ctc gac aag atg gtc ggg gat tat cac ttc acc Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr 515 520 525	1584		
tgc aac gtg aac gag ttc gcc cag cgg tac gcc gag gag ggc aac aat Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn 530 535 540	1632		
gtg ttc atg tac ctg tac acg cac aga agc aaa gga aat ccc tgg ccg Val Phe Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro 545 550 555 560	1680		
agg tgg act ggc gtg atg cac ggc gac gag atc aac tac gtg ttt ggc Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly 565 570 575	1728		
gaa ccg ctg aac tcg gcc ctc ggc tac cag gac gac gag aag gac ttt	1776		

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Glu Pro Leu Asn Ser Ala Leu Gly Tyr Gln Asp Asp Glu Lys Asp Phe
580 585 590

agc cgg aaa att atg cga tac tgg tcc aac ttt gcc aag act ggc aat 1824
Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn
595 600 605

cca aac ccg agt acg ccg agc gtg gac ctg ccc gaa tgg ccc aag cac 1872
Pro Asn Pro Ser Thr Pro Ser Val Asp Leu Pro Glu Trp Pro Lys His
610 615 620

acc gcc cac gga cga cac tat ctg gag ctg gga ctg aac acg acc ttc 1920
Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Thr Phe
625 630 635

gtg gga cgg ggc cca cga ttg cgg cag tgc gct ttc tgg aag aaa tat 1968
Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr
645 650 655

ttg ccg caa cta gta gca gct acc tct aac ctc caa gta act ccc gcg 2016
Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Gln Val Thr Pro Ala
660 665 670

cct agc gta cct tgc gaa agc agc tca aca tct tat cga tcc act cta 2064
Pro Ser Val Pro Cys Glu Ser Ser Ser Thr Ser Tyr Arg Ser Thr Leu
675 680 685

ctt cta ata gtc aca cta ctt tta gta acg cgg ttc aag att taa 2109
Leu Leu Ile Val Thr Leu Leu Leu Val Thr Arg Phe Lys Ile
690 695 700

<210> 57

<211> 702

<212> PRT

<213> Culex pipiens strain SR

<400> 57

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Arg His Leu Ile Leu Cys Ser Leu Gly Leu Tyr Ser Ile Leu Val Gln
20 25 30

Ser Val His Cys Arg His His Asp Ile Gly Ser Ser Val Ala His Gln
35 40 45

Leu Gly Ser Lys Tyr Ser Gln Ser Ser Ser Leu Ser Ser Ser Gln
50 55 60

Ser Ser Ser Ser Leu Ala Glu Glu Ala Thr Leu Asn Lys Asp Ser Asp
65 70 75 80

Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Asp Ser Val Arg Ile Val
85 90 95

Asp Ala Glu Leu Gly Thr Leu Glu Arg Glu His Ile His Ser Thr Thr
100 105 110

Thr Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Ser Ser Asp Ala Thr
115 120 125

Asp Ser Asp Pro Leu Val Ile Thr Thr Asp Lys Gly Lys Ile Arg Gly

130

135

140

Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly
 145 150 155 160
 Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro
 165 170 175
 Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro
 180 185 190
 Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly
 195 200 205
 Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr
 210 215 220
 Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met
 225 230 235 240
 Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp
 245 250 255
 Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val
 260 265 270
 Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr
 275 280 285
 Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu
 290 295 300
 Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg
 305 310 315 320
 Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His
 325 330 335
 Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln
 340 345 350
 Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala
 355 360 365
 Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Asn Cys Pro His Asp
 370 375 380
 Ala Thr Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Thr Lys Asp Pro
 385 390 395 400
 Asn Glu Leu Val Asp Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe
 405 410 415
 Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln
 420 425 430
 Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Asp Ile Leu Thr Gly
 435 440 445
 Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu
 450 455 460
 Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu

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465          470          475          480
Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln
          485          490          495
Ala Ile Val Phe Glu Tyr Thr Asp Trp Ile Glu Pro Asp Asn Pro Asn
          500          505          510
Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr
          515          520          525
Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn
          530          535          540
Val Phe Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro
          545          550          555
Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly
          565          570          575
Glu Pro Leu Asn Ser Ala Leu Gly Tyr Gln Asp Asp Glu Lys Asp Phe
          580          585          590
Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn
          595          600          605
Pro Asn Pro Ser Thr Pro Ser Val Asp Leu Pro Glu Trp Pro Lys His
          610          615          620
Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Thr Phe
          625          630          635
Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr
          645          650          655
Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Gln Val Thr Pro Ala
          660          665          670
Pro Ser Val Pro Cys Glu Ser Ser Ser Thr Ser Tyr Arg Ser Thr Leu
          675          680          685
Leu Leu Ile Val Thr Leu Leu Leu Val Thr Arg Phe Lys Ile
          690          695          700

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<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

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<220>
<223> synthetic DNA

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<400> 58
cgactcggac ccactggt

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18

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<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>

<223> synthetic DNA

<400> 59

gttctgatca aacagccccg c

21

<210> 60

<211> 459

<212> DNA

<213> Culex pipiens pipiens strain Espro (R)

<220>

<221> CDS

<222> (3)..(458)

<400> 60

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 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 80 85 90 95

aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc 335
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser
 100 105 110

ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

ttt ctc ttc ctg ggc aca ccg gag gca c 459
 Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 61

<211> 461

<212> DNA

<213> Culex pipiens quinquefasciatus strain ProR(S)

<220>

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<221> CDS

<222> (3)..(458)

<400> 61

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ac aag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag      47
  Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
    1             5             10             15

aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt      95
  Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
                20             25             30

ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg     143
  Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
                35             40             45

ctg aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc     191
  Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
                50             55             60

gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg     239
  Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
                65             70             75

ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca ccg ccc agg     287
  Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
                80             85             90

ccc aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt gcc ttc tac     335
  Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr
                100            105            110

tcc ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg     383
  Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
                115            120            125

gag gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt     431
  Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
                130            135            140

ggg ttt ctc ttc ctg ggc aca ccg gag gca                               461
  Gly Phe Leu Phe Leu Gly Thr Pro Glu
                145            150

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<210> 62

<211> 448

<212> DNA

<213> Culex pipiens pipiens strain S-LAB (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 62

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  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
    1             5             10             15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg      95
  Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20             25             30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg     143

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263365us-seq-list-082310 (2).txt

Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45

aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca ccg ccc agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
80 85 90 95

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg act gcc acg ctg gac gtg tac gac cac ccg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggg 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140

ttt ctc ttc ctg ggc ac 448
Phe Leu Phe Leu Gly
145

<210> 63

<211> 459

<212> DNA

<213> Culex pipiens pipiens strain Padova (R)

<220>

<221> CDS

<222> (3)..(458)

<400> 63

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Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30

ctc ccg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
Page 43

263365us-seq-list-082310 (2).txt

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80          85          90          95
aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser
100          105          110
ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115          120          125
gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130          135          140
ttt ctc ttc ctg ggc aca ccg gag gca c
Phe Leu Phe Leu Gly Thr Pro Glu Ala
145          150
<210> 64
<211> 463
<212> DNA
<213> Culex pipiens pipiens strain Praias (R)
<220>
<221> CDS
<222> (1)..(462)
<400> 64
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Asp Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
1          5          10          15
aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt 96
Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
20          25          30
ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg 144
Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
35          40          45
ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc 192
Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
50          55          60
gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc 240
Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
65          70          75          80
ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg 288
Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
85          90          95
ccc aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac 336
Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
100          105          110
tcc ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg 384
Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
115          120          125
gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt 432

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Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
 130 135 140

ggt ttt ctc ttc ctg ggc aca ccg gag gca c 463
 Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 65

<211> 463

<212> DNA

<213> Culex pipiens quinquefasciatus strain Supercar (R)

<220>

<221> CDS

<222> (1)..(462)

<400> 65

gac aag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag 48
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 1 5 10 15

aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt 96
 Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 20 25 30

ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg 144
 Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
 35 40 45

ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc 192
 Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
 50 55 60

gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc 240
 Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
 65 70 75 80

ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg 288
 Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
 85 90 95

ccc aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac 336
 Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
 100 105 110

tcc ggg act gcc acg ttg gac gtg tac gat cat ccg acg ctg gcc tcg 384
 Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
 115 120 125

gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt 432
 Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
 130 135 140

ggt ttt ctc ttc ctg ggc aca ccg gag gca c 463
 Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 66

<211> 448

<212> DNA

<213> Culex pipiens pipiens strain Bruges A (S)

<220>

263365us-seq-list-082310 (2).txt

<221> CDS

<222> (3)..(446)

<400> 66

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ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag      47
  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
    1           5           10           15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg      95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
          20           25           30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg     143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
          35           40           45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg     191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
          50           55           60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc     239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
          65           70           75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc     287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
          80           85           90           95

aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt ggc ttc tac tcc     335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
          100           105           110

ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag     383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
          115           120           125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt     431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
          130           135           140

ttt ctc ttc ctg ggc ac
Phe Leu Phe Leu Gly
          145

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<210> 67

<211> 457

<212> DNA

<213> Culex pipiens quinquefasciatus strain BO (R)

<220>

<221> CDS

<222> (1)..(456)

<400> 67

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ggc aaa atc cgt gga acg aca ctg gaa gcg cct agc gga aag aag gtg      48
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
  1           5           10           15

gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc      96
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
          20           25           30

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263365us-seq-list-082310 (2).txt

cg	g	t	t	c	a	c	a	t	c	c	c	g	a	a	a	t	g	a	c	g	g	t	g	c	t	a	a	c		144	
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn																
		35					40					45																			
g	c	a	a	a	c	c	a	a	c	t	c	t	g	c	a	a	c	a	t	g	g	a	c	c	g	t	t	c		192	
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe																
		50				55					60																				
g	g	t	a	c	c	g	g	g	a	c	a	t	g	t	g	a	a	c	c	g	a	a	c	a	c	c	t	c		240	
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser																
		65			70				75						80																
g	a	g	a	c	c	t	a	c	a	a	c	g	t	g	c	a	c	c	g	a	a	c	a	c	a	c	c	a	a		288
Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys																
				85				90						95																	
a	a	t	g	c	c	c	g	t	a	c	t	g	t	g	a	t	t	c	g	g	g	a	c	t	t	c	c	g		336	
Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Ser	Phe	Tyr	Ser	Gly																
			100				105					110																			
a	c	t	g	c	c	a	c	c	g	a	c	c	t	g	g	c	c	t	g	g	a	c	c	t	g	g	a	g		384	
Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu																
		115				120					125																				
a	a	c	g	t	a	c	g	t	a	c	c	g	t	g	c	a	a	g	t	t	g	g	t	t	t	t	t		432		
Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe																
		130			135					140																					
c	t	c	t	c	g	a	c	a	c	c	g	a	g	a	c															457	
Leu	Phe	Leu	Gly	Thr	Pro	Glu	Ala																								
		145			150																										

<210> 68

<211> 447

<212> DNA

<213> Culex pipiens quinquefasciatus strain DJI (R)

<220>

<221> CDS

<222> (1)..(444)

<400> 68

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Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val																				
		1		5				10					15																						
g	a	c	g	a	t	g	g	c	a	t	t	c	c	g	t	a	c	g	c	a	c	c	t	c	c	g	c	t	g	g	t	c	c		96
Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu																				
			20			25						30																							
c	g	t	t	c	a	c	c	g	a	a	c	c	g	a	a	a	t	g	a	a	c	a	c	c	g	a	a	c	a	a	c	c		144	
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn																				
		35				40					45																								
g	c	a	a	a	c	c	a	a	c	t	c	t	g	c	a	a	c	a	t	g	g	a	c	c	g	a	a	c	a	a	c	c		192	
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe																				
		50			55				60																										
g	g	t	a	c	c	g	g	g	a	c	a	t	g	t	g	a	a	c	c	g	a	a	c	a	c	c	c	t	c	t	c		240		
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser																				
		65			70				75					80																					

263365us-seq-list-082310 (2).txt

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gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag 288
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85 90 95

aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt agc ttc tac tcc ggg 336
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110

act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag gag 384
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125

aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt 432
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

ctc ttc ctg ggc aca 447
Leu Phe Leu Gly
145

<210> 69
<211> 457
<212> DNA
<213> Culex pipiens quinquefasciatus strain Harare (R)

<220>
<221> CDS
<222> (1)..(456)

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gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc 96
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30

cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg aac 144
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45

gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg ttc 192
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60

ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc tcg 240
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80

gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag 288
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95

aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt agc ttc tac tcc ggg 336
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110

act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag gag 384
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125

aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt 432

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263365us-seq-list-082310 (2).txt

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

ctc ttc ctg ggc aca ccg gag gca c
Leu Phe Leu Gly Thr Pro Glu Ala
145 150

457

<210> 70

<211> 458

<212> DNA

<213> Culex pipiens quinquefasciatus strain Martinique (R)

<220>

<221> CDS

<222> (1)..(456)

<400> 70

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1 5 10 15

gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc 96
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30

cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg aac 144
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45

gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg ttc 192
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60

ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc tcg 240
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80

gag gac tgt ctg tac atc aac gtg gtc gtg cca ccg ccc agg ccc aag 288
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95

aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt agc ttc tac tcc ggg 336
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110

act gcc acg ctg gac gtg tac gac cac ccg acg ctg gcc tcg gag gag 384
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125

aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt 432
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

ctc ttc ctg ggc aca ccg gag gca cc 458
Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 71

<211> 447

<212> DNA

<213> Culex pipiens pipiens strain Barriol (R)

<220>

263365us-seq-list-082310 (2).txt

<221> CDS

<222> (3)..(446)

<400> 71

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   1           5           10
gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20           25           30
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
                35           40           45
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
                50           55           60
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
                65           70           75
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
   80           85           90           95
aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser
                100           105           110
ggg act gcc acg ttg gac gtg tac gat cat ccg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
                115           120           125
gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
                130           135           140
ttt ctc ttc ctg ggc a
Phe Leu Phe Leu Gly
   145

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<210> 72

<211> 447

<212> DNA

<213> Culex pipiens pipiens strain Bleuete (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 72

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ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag 47
  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
   1           5           10
gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20           25           30
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143

```

263365us-seq-list-082310 (2).txt

```

Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
      35      40      45
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
      50      55      60
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
      65      70      75
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
      80      85      90      95
aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
      100      105      110
ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
      115      120      125
gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
      130      135      140
ttt ctc ttc ctg ggc a
Phe Leu Phe Leu Gly
      145
<210> 73
<211> 448
<212> DNA
<213> Culex pipiens pipiens strain Bruges B (S)
<220>
<221> CDS
<222> (3)..(446)
<400> 73
ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag 47
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
      1      5      10      15
gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
      20      25      30
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
      35      40      45
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
      50      55      60
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
      65      70      75

```

263365us-seq-list-082310 (2).txt

```

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
80 85 90 95

aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140

ttt ctc ttc ctg ggc ac 448
Phe Leu Phe Leu Gly
145

<210> 74
<211> 447
<212> DNA
<213> Culex pipiens pipiens strain Heteren (S)

<220>
<221> CDS
<222> (3)..(446)

<400> 74
ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag 47
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30

ctc cgg ttt cga cat cca cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac aca gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
80 85 90 95

aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg act gcc acg ttg gac gtg tac gac cat cgg acg ctg gcc tcg gaa 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431

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Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

ttt ctc ttc ctg ggc a
 Phe Leu Phe Leu Gly
 145

447

<210> 75

<211> 450

<212> DNA

<213> Culex pipiens quinquefasciatus strain Ling (S)

<220>

<221> CDS

<222> (1)..(447)

<400> 75

cag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 48
 Gln Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15

gtg gac gcc tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 96
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 144
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45

aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 192
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 240
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75 80

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 288
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 85 90 95

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 336
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110

ggg act gcc acg ctg gac gtg tat gac cac cgg acg ctg gcc tcg gag 384
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 432
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

ttt ctc ttc ctg ggc aca
 Phe Leu Phe Leu Gly
 145

450

<210> 76

<211> 448

<212> DNA

<213> Culex pipiens quinquefasciatus strain Mao (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 76

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ac ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag      47
  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
    1             5             10             15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg      95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20             25             30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg     143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
                35             40             45

aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg     191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
                50             55             60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc     239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
                65             70             75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc     287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
    80             85             90             95

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc     335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
                100             105             110

ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag     383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
                115             120             125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt     431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
                130             135             140

ttt ctc ttc ctg ggc ac                                             448
Phe Leu Phe Leu Gly
    145

```

<210> 77

<211> 433

<212> DNA

<213> Culex pipiens quinquefasciatus strain TemR (S)

<220>

<221> CDS

<222> (1)..(432)

<400> 77

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aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag gtg gac      48
Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp
    1             5             10             15

gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc cgg      96
Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg
                20             25             30

```

263365us-seq-list-082310 (2).txt

```

ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg 144
Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala
      35              40              45

acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg ttc ggt 192
Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly
      50              55              60

gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc tcg gag 240
Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu
      65              70              75

gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag aat 288
Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn
      85              90              95

gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc ggg act 336
Ala Ala Val Met Leu Trp Ile Phe Gly Gly Phe Tyr Ser Gly Thr
      100             105             110

gcc acg ctg gac gtg tac gac cac cgg acg ctg acc tcg gag gag aac 384
Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu Glu Asn
      115             120             125

gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt ctc t 433
Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
      130             135             140

<210> 78
<211> 448
<212> DNA
<213> Culex torrentium strain Uppsala

<220>
<221> CDS
<222> (3)..(446)

<400> 78
ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag 47
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
      1              5              10              15

gtg gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
      20              25              30

ctt cgg ttt cga cat cca cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
      35              40              45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtc gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
      50              55              60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
      65              70              75

tcg gaa gac tgt ctg tac atc aac gtt gtg gtg cca cgg ccg agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
      80              85              90              95

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263365us-seq-list-082310 (2).txt

```

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt gga ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg acc gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140

ttt ctc ttc ctg ggc ac 448
Phe Leu Phe Leu Gly
145

<210> 79
<211> 448
<212> DNA
<213> Culex pipiens quinquefasciatus strain Trans (S)

<220>
<221> CDS

<222> (3)..(446)

<400> 79
ag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 47
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
80 85 90 95

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg acc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu
115 120 125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140

```

ttt ctc ttc ctg ggc ac
Phe Leu Phe Leu Gly
145

<210> 80
<211> 412
<212> DNA
<213> Culex pipiens quinquefasciatus strain BED (S)

<220>
<221> CDS
<222> (1)..(411)

<400> 80
aca ctg gaa gcg cct agt gga aag aag gtg gac gca tgg atg ggc att 48
Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1 5 10 15
ccg tac gcg cag cct ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 96
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20 25 30
ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa cca ccc aac 144
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35 40 45
tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc 192
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50 55 60
acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc 240
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65 70 75 80
aac gtg gtc gtg cca ccg ccc agg ccc aag aat gcc gcc gtc atg ctg 288
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
85 90 95
tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg 336
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100 105 110
tac gac cac ccg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg 384
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125
ctg cag tac cgt gtc gca agt ctt ggt t 412
Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135

<210> 81
<211> 437
<212> DNA
<213> Culex pipiens quinquefasciatus strain BSQ (S)

<220>
<221> CDS
<222> (3)..(434)

<400> 81
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Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15

263365us-seq-list-082310 (2).txt

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gtg gac gcc tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20                25                30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
                35                40                45

aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
                50                55                60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
                65                70                75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
                80                85                90

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
                100                105                110

ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
                115                120                125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggg 431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
                130                135                140

ttt ctc 437
Phe

<210> 82
<211> 414
<212> DNA
<213> Culex pipiens quinquefasciatus strain Brazza (S)

<220>
<221> CDS
<222> (2)..(412)

<400> 82
a ctg gaa gcg cct agt gga aag aag gtg gac gcc tgg atg ggc att ccg 49
  Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
    1                5                10                15

tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc 97
Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
                20                25                30

gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac tcc 145
Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
                35                40                45

tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc acc 193
Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
                50                55                60

atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc aac 241

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263365us-seq-list-082310 (2).txt

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
65 70 75 80

gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg tgg 289
Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85 90 95

atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg tac 337
Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
100 105 110

gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg ctg 385
Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
115 120 125

cag tac cgt gtc gca agt ctt ggg ttt ct 414
Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135

<210> 83

<211> 437

<212> DNA

<213> Culex pipiens quinquefasciatus strain Bouake (R)

<220>

<221> CDS

<222> (3)..(434)

<400> 83

ag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 47
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45

aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
80 85 90 95

aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt gcc ttc tac tcc 335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110

ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125

gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
Page 59

Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

ttt ctc
 Phe

437

<210> 84
 <211> 416

<212> DNA

<213> Culex pipiens quinquefasciatus strain Thai (S)

<220>

<221> CDS

<222> (1)..(414)

<400> 84

aca ctg gaa gcg cct agt gga aag aag gtg gac gcc tgg atg ggc att 48
 Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
 1 5 10 15

ccg tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 96
 Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
 20 25 30

ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac 144
 Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
 35 40 45

tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc 192
 Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
 50 55 60

acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc 240
 Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
 65 70 75 80

aac gtg gtc gtg cca ccg ccc agg ccc aag aat gcc gcc gtc atg ctg 288
 Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
 85 90 95

tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg 336
 Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
 100 105 110

tac gac cac ccg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg 384
 Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
 115 120 125

ctg cag tac cgt gtc gca agt ctt ggg ttt ct 416
 Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135

<210> 85

<211> 426

<212> DNA

<213> Culex pipiens quinquefasciatus strain Madurai (S)

<220>

<221> CDS

<222> (3)..(425)

<400> 85

ca ctg gaa gcg cct agt gga aag aag gtg gac gca tgg atg ggc att 47
 Page 60

263365us-seq-list-082310 (2).txt

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Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1      5      10      15
ccg tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 95
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20      25      30
ccc gcc gaa aga tgg acc ggt gtg ctg aac gca acc aaa ccg ccc aac 143
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35      40      45
tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc 191
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50      55      60
acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc 239
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65      70      75
aac gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg 287
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
80      85      90
tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg 335
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100      105      110
tac gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg 383
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115      120      125
ctg cag tac cgt gtc gca agt ctt ggg ttt ctc ttc ctg ggc a 426
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
130      135      140

<210> 86
<211> 423
<212> DNA
<213> Culex pipiens quinquefasciatus strain Recife (R)

<220>
<221> CDS
<222> (1)..(423)

<400> 86
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tac gcg cag cct ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc 96
Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
20      25      30
gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac tcc 144
Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
35      40      45
tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc acc 192
Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
50      55      60
atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc aac 240

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263365us-seq-list-082310 (2).txt

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Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
65          70          75          80

gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg tgg 288
Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85          90

atc ttc ggg ggt agc ttc tac tcc ggg act gcc acg ctg gac gtg tac 336
Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
100        105        110

gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg ctg 384
Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
115        120        125

cag tac cgt gtc gca agt ctt ggt ttt ctc ttc ctg ggc 423
Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
130        135        140

<210> 87
<211> 416
<212> DNA
<213> Culex pipiens quinquefasciatus strain Brasil (S)

<220>
<221> CDS
<222> (3)..(413)

<400> 87
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1          5          10

ccg tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 95
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20        25        30

ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac 143
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35        40        45

tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc 191
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50        55        60

acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc 239
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65          70          75

aac gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg 287
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
80          85          90

tgg atc ttc ggg ggt ggc ttc tat tcc ggg act gcc acg ctg gac gtg 335
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100        105        110

tac gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg 383
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115        120        125

ctg cag tac cgt gtc gca agt ctt ggg ttt ctc 416
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe

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130

<210> 88
<211> 418
<212> DNA
<213> Culex pipiens quinquefasciatus strain Moorea (S)

<220>
<221> CDS
<222> (1)..(417)

<400> 88
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Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
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ccg tac gcg cag cct ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 96
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20 25 30
ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac 144
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35 40 45
tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc 192
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50 55 60
acc atg tgg aac ccg aac aca ccg ctc tgc gag gac tgt ctg tac atc 240
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65 70 75 80
aac gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg 288
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
85 90 95
tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg 336
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100 105 110
tac gac cac cgg acg ctg gcc tgc gag gag aac gtg atc gta gtt tgc 384
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125
ctg cag tac cgt gtc gca agt ctt ggg ttt ctc t 418
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
130 135

<210> 89
<211> 402
<212> DNA
<213> Culex pipiens pipiens strain Killcare (S)

<220>
<221> CDS
<222> (1)..(402)

<400> 89
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Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro
1 5 10 15
ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg 96
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Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp
 20 25 30
 acc ggt gtg ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc 144
 Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile
 35 40 45
 gtg gac aca gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg 192
 Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro
 50 55 60
 aac aca ccc ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca 240
 Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro
 65 70 75 80
 agg ccg agg ccc aag aat gcc gct gtc atg ctg tgg atc ttc ggg ggt 288
 Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly
 85 90 95
 ggc ttc tac tcc ggg act gcc acg ttg gac gtg tac gat cat cgg acg 336
 Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr
 100 105 110
 ctg gcc tcg gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc 384
 Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val
 115 120 125
 gca agt ctt ggt ttt ctc 402
 Ala Ser Leu Gly Phe Leu
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<210> 90

<211> 152

<212> PRT

<213> Culex pipiens pipiens strain Espro (R)

<400> 90

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
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 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 91

<211> 152

<212> PRT

<213> Culex pipiens quinquefasciatus strain ProR(S)

<400> 91

Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15

Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30

Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45

Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60

Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75 80

Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 85 90 95

Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110

Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125

Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

Phe Leu Phe Leu Gly Thr Pro Glu
 145 150

<210> 92

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain S-LAB (S)

<400> 92

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15

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 20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80

263365us-seq-list-082310 (2).txt

Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 93
<211> 152
<212> PRT
<213> Culex pipiens pipiens strain Padova (R)

<400> 93
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1 5 10 15
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 94
<211> 154
<212> PRT
<213> Culex pipiens pipiens strain Praias (R)

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Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
20 25 30

263365us-seq-list-082310 (2).txt

Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
35 40 45
Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
50 55 60
Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
65 70 75 80
Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
85 90 95
Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
100 105 110
Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
115 120 125
Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
130 135 140
Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 95

<211> 154

<212> PRT

<213> *Culex pipiens quinquefasciatus* strain Supercar (R)

<400> 95

Asp Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
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Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
20 25 30
Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
35 40 45
Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
50 55 60
Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
65 70 75 80
Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
85 90 95
Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
100 105 110
Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
115 120 125
Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
130 135 140
Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 96

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Bruges A (S)

<400> 96

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
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<210> 97

<211> 152

<212> PRT

<213> Culex pipiens quinquefasciatus strain B0 (R)

<400> 97

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 Page 68

115

120

125

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 98

<211> 148

<212> PRT

<213> Culex pipiens quinquefasciatus strain DJI (R)

<400> 98

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80

Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95

Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110

Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

Leu Phe Leu Gly
 145

<210> 99

<211> 152

<212> PRT

<213> Culex pipiens quinquefasciatus strain Harare (R)

<400> 99

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 1 5 10 15

Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
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65											70											75											80
Glu	Asp	Cys	Leu	Tyr ₈₅	Ile	Asn	Val	Val	Val ₉₀	Pro	Arg	Pro	Arg	Pro ₉₅	Lys																		
Asn	Ala	Ala	Val ₁₀₀	Met	Leu	Trp	Ile	Phe ₁₀₅	Gly	Gly	Ser	Phe	Tyr ₁₁₀	Ser	Gly																		
Thr	Ala	Thr ₁₁₅	Leu	Asp	Val	Tyr	Asp ₁₂₀	His	Arg	Thr	Leu	Ala ₁₂₅	Ser	Glu	Glu																		
Asn	Val ₁₃₀	Ile	Val	Val	Ser	Leu ₁₃₅	Gln	Tyr	Arg	Val	Ala ₁₄₀	Ser	Leu	Gly	Phe																		
Leu ₁₄₅	Phe	Leu	Gly	Thr	Pro ₁₅₀	Glu	Ala																										

<210> 100

<211> 152

<212> PRT

<213> *Culex pipiens quinquefasciatus* strain Martinique (R)

<400> 1.00

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20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80

Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95

Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110

Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 101

<211>	148
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<212> PRT

<213> Culex pipiens pipiens strain Barriol (R)

<400> 101

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
Page 70

20

25

30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 102

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Bleuete (S)

<400> 102

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 103

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Bruges B (S)

<400> 103

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 104

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Heteren (S)

<400> 104

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125

115

120

125

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

Leu Phe Leu Gly
 145

<210> 105

<211> 149

<212> PRT

<213> Culex pipiens quinquefasciatus strain Ling (S)

<400> 105

Gln Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15

Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30

Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45

Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60

Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75 80

Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 85 90 95

Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110

Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125

Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

Phe Leu Phe Leu Gly
 145

<210> 106

<211> 148

<212> PRT

<213> Culex pipiens quinquefasciatus strain Mao (S)

<400> 106

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15

Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60

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Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 107

<211> 144

<212> PRT

<213> Culex pipiens quinquefasciatus strain TemR (S)

<400> 107

Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp
1 5 10 15
Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg
20 25 30
Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala
35 40 45
Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly
50 55 60
Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu
65 70 75 80
Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn
85 90 95
Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr
100 105 110
Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu Glu Asn
115 120 125
Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
130 135 140

<210> 108

<211> 148

<212> PRT

<213> Culex torrentium strain Uppsala

<400> 108

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
1 5 10 15
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30

263365us-seq-list-082310 (2).txt

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 109

<211> 148

<212> PRT

<213> Culex pipiens quinquefasciatus strain Trans (S)

<400> 109

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
1 5 10 15
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 110

<211> 137

<212> PRT

<213> Culex pipiens quinquefasciatus strain BED (S)

<400> 110

Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
 1 5 10 15
 Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
 20 25 30
 Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
 35 40 45
 Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
 50 55 60
 Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
 65 70 75 80
 Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
 85 90 95
 Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
 100 105 110
 Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
 115 120 125
 Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135

<210> 111

<211> 144

<212> PRT

<213> Culex pipiens quinquefasciatus strain BSQ (S)

<400> 111

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

<210> 112

<211> 137

<212> PRT

<213> Culex pipiens quinquefasciatus strain Brazza (S)

<400> 112

Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
 1 5 10 15

Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
 20 25 30

Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
 35 40 45

Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
 50 55 60

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
 65 70 75 80

Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
 85 90 95

Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
 100 105 110

Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
 115 120 125

Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135

<210> 113

<211> 144

<212> PRT

<213> Culex pipiens quinquefasciatus strain Bouake (R)

<400> 113

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15

Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30

Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45

Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80

Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95

Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110

Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125

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Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

<210> 114

<211> 138

<212> PRT

<213> Culex pipiens quinquefasciatus strain Thai (S)

<400> 114

Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1 5 10 15

Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20 25 30

Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35 40 45

Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50 55 60

Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65 70 75 80

Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
85 90 95

Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100 105 110

Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125

Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135

<210> 115

<211> 141

<212> PRT

<213> Culex pipiens quinquefasciatus strain Madurai (S)

<400> 115

Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
1 5 10 15

Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
20 25 30

Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
35 40 45

Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
50 55 60

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
65 70 75 80

Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85 90 95

Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
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100

105

110

Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
 115 120 125

Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
 130 135 140

<210> 116

<211> 141

<212> PRT

<213> Culex pipiens quinquefasciatus strain Recife (R)

<400> 116

Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
 1 5 10 15

Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
 20 25 30

Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
 35 40 45

Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
 50 55 60

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
 65 70 75 80

Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
 85 90 95

Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
 100 105 110

Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
 115 120 125

Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
 130 135 140

<210> 117

<211> 137

<212> PRT

<213> Culex pipiens quinquefasciatus strain Brasil (S)

<400> 117

Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
 1 5 10 15

Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
 20 25 30

Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
 35 40 45

Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
 50 55 60

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
 65 70 75 80

263365us-seq-list-082310 (2).txt

Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85 90 95
Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
100 105 110
Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
115 120 125
Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135

<210> 118

<211> 139

<212> PRT

<213> Culex pipiens quinquefasciatus strain Moorea (S)

<400> 118

Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1 5 10 15
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20 25 30
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35 40 45
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50 55 60
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65 70 75 80
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
85 90 95
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100 105 110
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
130 135

<210> 119

<211> 134

<212> PRT

<213> Culex pipiens pipiens strain killcare (S)

<400> 119

Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro
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Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp
20 25 30
Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile
35 40 45
Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro
50 55 60

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Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro
65 70 75 80
Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly
85 90 95
Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr
100 105 110
Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val
115 120 125
Ala Ser Leu Gly Phe Leu
130

<210> 120
<211> 2527
<212> DNA
<213> Anopheles gambiae strain YAO

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<210> 121
 <211> 2214
 <212> DNA
 <213> Anopheles gambiae strain YAO

<220>
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<400> 121
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 Met Val Pro Leu Gly Leu Leu Gly Val Thr Ala Leu Leu Leu Ile Leu
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 35 40 45
 gcc gcc atc gga tcg cat cag ctg tcg gct gcc gcc ggt gtt ggc ctt 192
 Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
 50 55 60
 tcc tcc cag tcc gcc cag tcc gga tcg ctc gca tcc ggt gtg atg tca 240
 Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
 65 70 75 80
 tcc gtt cct gct gcc gga gcg tca tcc tcc tcc tcg tcg tcg ctg ctg 288
 Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Ser Leu Leu
 85 90 95
 tca tcg tca gcc gag gac gac gtg gcg cgc att act ctc agc aag gac 336
 Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
 100 105 110
 gca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc gca cga 384
 Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Ala Arg
 115 120 125
 att ata gat gcc gag ttg ggc acg ctc gag cat gta cac agt gga gca 432
 Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
 130 135 140
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 Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
 145 150 155 160
 aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc atc cgc 528
 Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
 165 170 175
 ggc att acg gtc gat gcc ccc agc ggc aag aag gtg gac gtg tgg ctc 576
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 180 185 190

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210 215 220	
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Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro	
225 230 235 240	
ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac tgt ctg	768
Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu	
245 250 255	
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Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val	
260 265 270	
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275 280 285	
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Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val	
290 295 300	
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Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly	
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325 330 335	
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Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser	
340 345 350	
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Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu	
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cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag ccg gcc atc ctg	1152
His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu	
370 375 380	
cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc gag gaa	1200
Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu	
385 390 395 400	
gcc acg cta aga gca ctg ccg ttg gcc gag gcg gtc ggc tgc ccg cac	1248
Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His	
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gaa ccg agc aag ctg agc gat gcg gtc gag tgt ctg cgc ggc aag gat	1296
Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp	
420 425 430	
ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att tgc gag	1344
Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu	
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Gln	Arg	Ser	Leu	Ala	Ser	Gly	Arg	Phe	Lys	Lys	Thr	Glu	Ile	Leu	Thr	
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ggc	agc	aac	acg	gag	gag	ggc	tac	tac	ttc	atc	atc	tac	tac	ctg	acc	1488
Gly	Ser	Asn	Thr	Glu	Glu	Gly	Tyr	Tyr	Phe	Ile	Ile	Tyr	Tyr	Leu	Thr	
				485					490					495		
gag	ctg	ctg	cgc	aag	gag	gag	ggc	gtg	acc	gtg	acg	cgc	gag	gag	ttc	1536
Glu	Leu	Leu	Arg	Lys	Glu	Glu	Gly	Val	Thr	Val	Thr	Arg	Glu	Glu	Phe	
			500					505					510			
ctg	cag	gcg	gtg	cgc	gag	ctc	aac	ccg	tac	gtg	aac	ggg	gcg	gcc	cgg	1584
Leu	Gln	Ala	Val	Arg	Glu	Leu	Asn	Pro	Tyr	Val	Asn	Gly	Ala	Ala	Arg	
		515					520					525				
cag	gcg	atc	gtg	ttc	gag	tac	acc	gac	tgg	acc	gag	ccg	gac	aac	ccg	1632
Gln	Ala	Ile	Val	Phe	Glu	Tyr	Thr	Asp	Trp	Thr	Glu	Pro	Asp	Asn	Pro	
	530					535					540					
aac	agc	aac	cgg	gac	gcg	ctg	gac	aag	atg	gtg	ggc	gac	tat	cac	ttc	1680
Asn	Ser	Asn	Arg	Asp	Ala	Leu	Asp	Lys	Met	Val	Gly	Asp	Tyr	His	Phe	
					550					555					560	
acc	tgc	aac	gtg	aac	gag	ttc	gcg	cag	cgg	tac	gcc	gag	gag	ggc	aac	1728
Thr	Cys	Asn	Val	Asn	Glu	Phe	Ala	Gln	Arg	Tyr	Ala	Glu	Glu	Gly	Asn	
				565					570					575		
aac	gtc	tac	atg	tat	ctg	tac	acg	cac	cgc	agc	aaa	ggc	aac	ccg	tgg	1776
Asn	Val	Tyr	Met	Tyr	Leu	Tyr	Thr	His	Arg	Ser	Lys	Gly	Asn	Pro	Trp	
			580					585				590				
ccg	cgc	tgg	acg	ggc	gtg	atg	cac	ggc	gac	gag	atc	aac	tac	gtg	ttc	1824
Pro	Arg	Trp	Thr	Gly	Val	Met	His	Gly	Asp	Glu	Ile	Asn	Tyr	Val	Phe	
		595					600					605				
ggc	gaa	ccg	ctc	aac	ccc	acc	ctc	ggc	tac	acc	gag	gac	gag	aaa	gac	1872
Gly	Glu	Pro	Leu	Asn	Pro	Thr	Leu	Gly	Tyr	Thr	Glu	Asp	Glu	Lys	Asp	
	610					615					620					
ttt	agc	cgg	aag	atc	atg	cga	tac	tgg	tct	aac	ttt	gcc	aaa	acc	ggc	1920
Phe	Ser	Arg	Lys	Ile	Met	Arg	Tyr	Trp	Ser	Asn	Phe	Ala	Lys	Thr	Gly	
					630					635					640	
aat	cca	aat	ccc	aac	aca	gcc	agc	agc	gaa	ttc	ccc	gag	tgg	ccc	aag	1968
Asn	Pro	Asn	Pro	Asn	Thr	Ala	Ser	Ser	Glu	Phe	Pro	Glu	Trp	Pro	Lys	
				645					650					655		
cac	acc	gcc	cac	gga	cgg	cac	tat	ctg	gag	ctg	ggc	ctc	aac	acg	tcc	2016
His	Thr	Ala	His	Gly	Arg	His	Tyr	Leu	Glu	Leu	Gly	Leu	Asn	Thr	Ser	
			660					665				670				
ttc	gtc	ggg	cgg	ggc	cca	cgg	ttg	agg	cag	tgt	gcc	ttc	tgg	aag	aag	2064
Phe	Val	Gly	Arg	Gly	Pro	Arg	Leu	Arg	Gln	Cys	Ala	Phe	Trp	Lys	Lys	
		675					680					685				
tac	ctt	ccc	cag	cta	gtt	gca	gct	acc	tcg	aac	cta	cca	ggg	cca	gca	2112
Tyr	Leu	Pro	Gln	Leu	Val	Ala	Ala	Thr	Ser	Asn	Leu	Pro	Gly	Pro	Ala	

690
ccg ccc agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga cct gat 2160
Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Tyr Arg Pro Asp
705 710 715 720
ctg atc gtg ctg ctg gtg tgc ctg ctt acg gcg acc gtc aga ttc ata 2208
Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg Phe Ile
725 730 735
caa taa 2214
Gln

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<211> 737
<212> PRT
<213> Anopheles gambiae strain YAO

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Pro Pro Ser Ala Leu Val Gln Gly Arg His His Glu Leu Asn Asn Gly
35 40 45
Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
50 55 60
Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
65 70 75 80
Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Leu Leu
85 90 95
Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
100 105 110
Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Ala Arg
115 120 125
Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
130 135 140
Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
145 150 155 160
Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
165 170 175
Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu
180 185 190
Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His
195 200 205
Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro
210 215 220
Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro
Page 85

225 230 235 240
 Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu
 245 250 255
 Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val
 260 265 270
 Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu
 275 280 285
 Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val
 290 295 300
 Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
 305 310 315 320
 Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala
 325 330 335
 Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser
 340 345 350
 Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu
 355 360 365
 His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu
 370 375 380
 Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu
 385 390 395 400
 Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His
 405 410 415
 Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp
 420 425 430
 Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu
 435 440 445
 Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro
 450 455 460
 Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr
 465 470 475 480
 Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr
 485 490 495
 Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe
 500 505 510
 Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg
 515 520 525
 Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro
 530 535 540
 Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe
 545 550 555 560
 Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn

565

570

575

Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp
 580 585 590
 Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe
 595 600 605
 Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp
 610 615 620
 Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly
 625 630 635 640
 Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys
 645 650 655
 His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser
 660 665 670
 Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys
 675 680 685
 Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala
 690 695 700
 Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp
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 Gln

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 <213> Artificial Sequence

<220>
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<210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 124
 aggatggccc gctggaacag 20

<210> 125
 <211> 2214
 <212> DNA

<213> Anopheles gambiae strain KISUMU

<220>

<221> CDS

<222> (1)..(2214)

<400> 125

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atg gtt ccg ctg ggt ctg ctc ggc gtg acc gcg ctg cta cta atc ctg	96
Met Val Pro Leu Gly Leu Leu Gly Val Thr Ala Leu Leu Ile Leu	
20 25 30	
cca ccc tcc gcg ctg gtg cag ggc cgg cac cac gag ctc aac aat ggt	144
Pro Pro Ser Ala Leu Val Gln Gly Arg His His Glu Asn Asn Gly	
35 40 45	
gcc gcc atc gga tcg cat cag ctg tcg gct gcc gcc ggt gtt ggc ctt	192
Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu	
50 55 60	
tcc tcc cag tcc gcc cag tcc gga tcg ctc gca tcc ggt gtg atg tca	240
Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser	
65 70 75 80	
tcc gtt cct gct gcc gga gcg tca tcc tcc tcc tcg tcg tcg ctg ctg	288
Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Leu Leu	
85 90 95	
tca tcg tca gcc gag gac gac gtg gcg cgc att act ctc agc aag gac	336
Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp	
100 105 110	
gca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc gta cga	384
Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Val Arg	
115 120 125	
att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt gga gca	432
Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala	
130 135 140	
acg ccg cgg cga cgc ggt ctg acg agg cgc gag tcc aac tcg gac gcg	480
Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala	
145 150 155 160	
aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc atc cgc	528
Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg	
165 170 175	
ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg tgg ctc	576
Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu	
180 185 190	
ggc att ccc tac gcc cag ccg ccg gtc ggg ccg tta cgg ttc cgt cat	624
Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His	
195 200 205	
ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc aca ccg	672
Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro	
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Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro	
225 230 235 240	
ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac tgt ctg	768
Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu	
245 250 255	
tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg gcc gtc	816
Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val	
260 265 270	
atg ctg tgg atc ttc ggc ggc ggc ttc tac tcc ggc acc gcc acc ctg	864
Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu	
275 280 285	
gac gtg tac gac cac ccg gcg ctt gcg tcc gag gag aac gtg atc gtg	912
Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val	
290 295 300	
gtg tcc ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt ctc ggc	960
Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly	
305 310 315 320	
acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac ctt gcg	1008
Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala	
325 330 335	
cta cgc tgg gtg ccg gac aac att cac ccg ttc ggt ggt gat ccg tcc	1056
Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser	
340 345 350	
cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcc gtg tcc ctg	1104
Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu	
355 360 365	
cat ctg ctg tcc gcc ctg tcc cgc gat ctg ttc cag ccg gcc atc ctg	1152
His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu	
370 375 380	
cag agc ggc tcc ccg acg gca ccg tgg gca ttg gta tcc cgc gag gaa	1200
Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu	
385 390 395 400	
gcc acg cta aga gca ctg ccg ttg gcc gag gcg gtc gcc tgc ccg cac	1248
Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His	
405 410 415	
gaa ccg agc aag ctg agc gat gcg gtc gag tgt ctg cgc ggc aag gat	1296
Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp	
420 425 430	
ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att tgc gag	1344
Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu	
435 440 445	
ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag acg ccg	1392
Phe Pro Phe Val Pro Val Asp Gly Ala Phe Leu Asp Glu Thr Pro	
450 455 460	
cag cgt tcc ctc gcc agc ggg cgc ttc aag aag acg gag atc ctc acc	1440
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465	470	475	480	
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gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag gag ttc	Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe	500	505	1536
ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg gcc ccg	Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg	515	520	1584
cag gcg atc gtg ttc gag tac acc gac tgg acc gag ccg gac aac ccg	Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro	530	535	1632
aac agc aac cgc gac gcg ctg gac aag atg gtg ggc gac tat cac ttc	Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe	545	550	1680
acc tgc aac gtg aac gag ttc gcg cag cgg tac gcc gag gag ggc aac	Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn	565	570	1728
aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac ccg tgg	Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp	580	585	1776
ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac gtg ttc	Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe	595	600	1824
ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag aaa gac	Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp	610	615	1872
ttt agc cgg aag atc atg cga tac tgg tct aac ttt gcc aaa acc ggc	Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly	625	630	1920
aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg ccc aag	Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys	645	650	1968
cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac acg tcc	His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser	660	665	2016
ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg aag aag	Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys	675	680	2064
tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg cca gca	Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala	690	695	2112
ccg ccc agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga cct gat	Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp	705	710	2160
ctg atc gtg ctg ctg gtg tcg ctg ctt acg gcg acc gtc aga ttc ata				2208

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 725 730 735

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 Gln

2214

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 <211> 737
 <212> PRT
 <213> Anopheles gambiae

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 35 40 45
 Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
 50 55 60
 Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
 65 70 75 80
 Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Leu Leu
 85 90 95
 Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
 100 105 110
 Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Val Arg
 115 120 125
 Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
 130 135 140
 Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
 145 150 155 160
 Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
 165 170 175
 Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu
 180 185 190
 Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His
 195 200 205
 Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro
 210 215 220
 Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro
 225 230 235 240
 Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu
 245 250 255
 Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val
 260 265 270

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 Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val
 290 300
 Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
 305 310 315 320
 Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala
 325 330 335
 Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser
 340 345 350
 Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu
 355 360 365
 His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu
 370 375 380
 Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu
 385 390 395 400
 Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His
 405 410 415
 Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp
 420 425 430
 Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu
 435 440 445
 Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro
 450 455 460
 Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr
 465 470 475 480
 Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr
 485 490 495
 Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe
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 Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg
 515 520 525
 Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro
 530 535 540
 Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe
 545 550 555 560
 Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn
 565 570 575
 Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp
 580 585 590
 Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe
 595 600 605

263365us-seq-list-082310 (2).txt

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Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly
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Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys
645 650 655

His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser
660 665 670

Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys
675 680 685

Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala
690 695 700

Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp
705 710 715 720

Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg Phe Ile
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Gln

<210> 127
<211> 10700
<212> DNA
<213> Anopheles gambiae

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263365us-seq-list-082310 (2).txt

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263365us-seq-list-082310 (2).txt

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245

250

255

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Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp
610 615 620

Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly
625 630 635 640

Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys
645 650 655

His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser
660 665 670

Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys
675 680 685

Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala
690 695 700

Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp
705 710 715 720

Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg Phe Ile
725 730 735

Gln

<210> 132
<211> 676
<212> PRT
<213> Schizaphis graminum

<400> 132

Met Asp Gln Trp Leu Leu Trp Phe Gly Tyr Leu Val Ala Ser Thr Tyr
1 5 10 15

263365us-seq-list-082310 (2).txt

Gly Leu Ser Leu Arg His Ala Arg His Gln Ser Val Gly Thr Pro Thr
20 25 30

Ala Glu Glu Ile Leu Glu Pro Gln Ile Leu Ile Glu Asp Thr Asp His
35 40 45

Val Phe Arg Gln Arg Ala Ser Asp Met Phe Ala Gln Glu Pro Glu Tyr
50 55 60

Thr Glu Lys Arg Asn Leu Asn His Arg Arg Arg Ser Glu Phe Ser Gly
65 70 75 80

Asn Gln Asp Thr Asp Phe Ala Ser Ser Gly Glu Thr Tyr Ser Ala Tyr
85 90 95

Thr Ser Asp Asp Pro Leu Ile Ile His Thr Asn Lys Gly Lys Ile Arg
100 105 110

Gly Ile Thr Gln Thr Ala Thr Thr Gly Lys Leu Val Asp Ala Trp Leu
115 120 125

Gly Ile Pro Tyr Ala Lys Lys Pro Ile Gly Asp Leu Arg Phe Arg His
130 135 140

Pro Arg Pro Ile Asp Arg Trp Asp Thr Thr Thr Pro Glu Thr Ile Leu
145 150 155 160

Asn Cys Thr Thr Pro Pro Asn Thr Cys Val Gln Ile Phe Asp Thr Leu
165 170 175

Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Ser Pro Val
180 185 190

Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Lys Pro Arg Pro
195 200 205

Gln Asn Ala Ala Val Met Val Trp Ile Phe Gly Gly Gly Phe Tyr Ser
210 215 220

Gly Ser Ala Thr Leu Asp Ile Tyr Asp Pro Lys Ile Leu Val Ser Glu
225 230 235 240

Glu Asn Val Ile Leu Val Ser Met Gln Tyr Arg Val Ala Ser Leu Gly
245 250 255

Phe Leu Tyr Phe Asp Thr Glu Asp Val Pro Gly Asn Ala Gly Leu Phe
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Asp Gln Leu Met Ala Leu Gln Trp Val His Glu Asn Ile Lys Leu Phe
275 280 285

Gly Gly Asn Pro Asn Asn Val Thr Leu Phe Gly Glu Ser Ala Gly Ala
290 295 300

Val Ser Val Ser Leu His Leu Leu Ser Pro Leu Ser Arg Asn Leu Phe
305 310 315 320

Asn Gln Ala Ile Met Glu Ser Gly Ser Ser Thr Ala Pro Trp Ala Ile
325 330 335

Leu Ser Arg Glu Glu Ser Phe Asn Arg Gly Leu Lys Leu Ala Lys Ala
340 345 350

Met Gly Cys Pro Asp Asp Arg Asn Thr Ile His Lys Thr Val Glu Cys
355 360 365

Leu Arg Lys Ala Asn Ser Ser Val Met Val Glu Lys Glu Trp Asp His
370 375 380

Val Ala Ile Cys Phe Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe
385 390 395 400

Leu Asp Asp His Pro Gln Lys Ser Leu Ser Thr Asn Asn Phe Lys Lys
405 410 415

Thr Asn Ile Leu Met Gly Ser Asn Ser Glu Glu Gly Tyr Tyr Ser Ile
420 425 430

Phe Tyr Tyr Leu Thr Glu Leu Phe Lys Lys Glu Glu Asn Val Met Val
435 440 445

Ser Arg Glu Asn Phe Ile Lys Ala Ile Gly Gln Leu Asn Pro Asn Ala
450 455 460

Asp Ala Ala Val Lys Ser Ala Ile Glu Phe Glu Tyr Thr Asp Trp Phe
465 470 475 480

Ser Pro Asn Asp Pro Glu Lys Asn Arg Asn Ala Leu Asp Lys Met Val
485 490 495

Gly Asp Tyr Gln Phe Thr Cys Asn Val Asn Glu Phe Ala His Lys Tyr
500 505 510

263365us-seq-list-082310 (2).txt

Ala Leu Thr Gly Asn Asn Val Tyr Met Tyr Tyr Phe Lys His Arg Ser
515 520 525

Leu Asn Asn Pro Trp Pro Lys Trp Thr Gly Val Met His Gly Asp Glu
530 535 540

Ile Ser Tyr Val Phe Gly Asp Pro Leu Asn Pro Asn Lys Arg Tyr Glu
545 550 555 560

Ile Glu Glu Ile Glu Leu Ser Lys Lys Met Met Arg Tyr Trp Thr Asn
565 570 575

Phe Ala Lys Thr Gly Asn Pro Ser Lys Thr Leu Glu Gly Ser Trp Val
580 585 590

Thr Pro Lys Trp Pro Val His Thr Ala Tyr Gly Lys Glu Phe Leu Thr
595 600 605

Leu Asp Thr Asn Asn Thr Ser Ile Gly Val Gly Pro Arg Leu Glu Gln
610 615 620

Cys Ala Phe Trp Lys Asn Tyr Val Pro Asp Leu Thr Ala Ile Ser Lys
625 630 635 640

Ser Met Lys Ser Asp Lys Asn Cys Thr Thr Ile Ser Gly Gly Thr Lys
645 650 655

Thr Asn Val Ile Glu Leu Ser Val Trp Thr Ile Val Met Thr Thr Ala
660 665 670

Val Leu Met Leu
675

<210> 133
<211> 645
<212> PRT
<213> Anopheles gambiae

<400> 133

Met Ala Ser Ala Tyr Tyr His Gln Ser Ala Val Gly Val Gly Asn Val
1 5 10 15

Leu Val Leu Leu Leu Gly Ala Thr Val Ile Cys Pro Ala Tyr Ala Ile
20 25 30

Ile Asp Arg Leu Val Val Gln Thr Ser Ser Gly Pro Ile Arg Gly Arg
35 40 45

Ser Thr Met Val Gln Gly Arg Glu Val His Val Phe Asn Gly Val Pro
 50 55 60

Phe Ala Lys Pro Pro Val Asp Ser Leu Arg Phe Lys Lys Pro Val Pro
 65 70 75 80

Ala Glu Pro Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro Pro Ser
 85 90 95

Cys Ile Gln Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ala Gly Glu Glu
 100 105 110

Met Trp Asn Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Tyr Leu Asn
 115 120 125

Ile Trp Val Pro Thr Lys Thr Arg Leu Arg His Gly Arg Gly Leu Asn
 130 135 140

Phe Gly Ser Asn Asp Tyr Phe Gln Asp Asp Asp Asp Phe Gln Arg Gln
 145 150 155 160

His Gln Ser Lys Gly Gly Leu Ala Met Leu Val Trp Ile Tyr Gly Gly
 165 170 175

Gly Phe Met Ser Gly Thr Ser Thr Leu Asp Ile Tyr Asn Ala Glu Ile
 180 185 190

Leu Ala Ala Val Gly Asn Val Ile Val Ala Ser Met Gln Tyr Arg Val
 195 200 205

Gly Ala Phe Gly Phe Leu Tyr Leu Ala Pro Tyr Ile Asn Gly Tyr Glu
 210 215 220

Glu Asp Ala Pro Gly Asn Met Gly Met Trp Asp Gln Ala Leu Ala Ile
 225 230 235 240

Arg Trp Leu Lys Glu Asn Ala Lys Ala Phe Gly Gly Asp Pro Asp Leu
 245 250 255

Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ser Ser Val Ser Leu His
 260 265 270

Leu Leu Ser Pro Val Thr Arg Gly Leu Ser Lys Arg Gly Ile Leu Gln
 275 280 285

Ser Gly Thr Leu Asn Ala Pro Trp Ser His Met Thr Ala Glu Lys Ala
 290 295 300

263365us-seq-list-082310 (2).txt

Leu Gln Ile Ala Glu Gly Leu Ile Asp Asp Cys Asn Cys Asn Leu Thr
305 310 315 320

Met Leu Lys Glu Ser Pro Ser Thr Val Met Gln Cys Met Arg Asn Val
325 330 335

Asp Ala Lys Thr Ile Ser Val Gln Gln Trp Asn Ser Tyr Ser Gly Ile
340 345 350

Leu Gly Phe Pro Ser Ala Pro Thr Ile Asp Gly Val Phe Met Thr Ala
355 360 365

Asp Pro Met Thr Met Leu Arg Glu Ala Asn Leu Glu Gly Ile Asp Ile
370 375 380

Leu Val Gly Ser Asn Arg Asp Glu Gly Thr Tyr Phe Leu Leu Tyr Asp
385 390 395 400

Phe Ile Asp Tyr Phe Glu Lys Asp Ala Ala Thr Ser Leu Pro Arg Asp
405 410 415

Lys Phe Leu Glu Ile Met Asn Thr Ile Phe Asn Lys Ala Ser Glu Pro
420 425 430

Glu Arg Glu Ala Ile Ile Phe Gln Tyr Thr Gly Trp Glu Ser Gly Asn
435 440 445

Asp Gly Tyr Gln Asn Gln His Gln Val Gly Arg Ala Val Gly Asp His
450 455 460

Phe Phe Ile Cys Pro Thr Asn Glu Phe Ala Leu Gly Leu Thr Glu Arg
465 470 475 480

Gly Ala Ser Val His Tyr Tyr Tyr Phe Thr His Arg Thr Ser Thr Ser
485 490 495

Leu Trp Gly Glu Trp Met Gly Val Leu His Gly Asp Glu Val Glu Tyr
500 505 510

Ile Phe Gly Gln Pro Met Asn Ala Ser Leu Gln Tyr Arg Gln Arg Glu
515 520 525

Arg Asp Leu Ser Arg Arg Met Val Leu Ser Val Ser Glu Phe Ala Arg
530 535 540

Thr Gly Asn Pro Ala Leu Glu Gly Glu His Trp Pro Leu Tyr Thr Arg
545 550 555 560

263365us-seq-list-082310 (2).txt

Glu Asn Pro Ile Tyr Phe Ile Phe Asn Ala Glu Gly Glu Asp Asp Leu
565 570 575

Arg Gly Glu Lys Tyr Gly Arg Gly Pro Met Ala Thr Ser Cys Ala Phe
580 585 590

Trp Asn Asp Phe Leu Pro Arg Leu Arg Ala Trp Ser Val Pro Leu Lys
595 600 605

Asp Pro Cys Lys Leu Asp Asp His Thr Ser Ile Ala Ser Thr Ala Arg
610 615 620

Ala Ala Pro Thr Val Ala Leu Leu Ile Ala Leu Ser Leu Ala Val Ala
625 630 635 640

Arg Leu Val Ala Ala
645

<210> 134
<211> 664
<212> PRT
<213> Anopheles stephensi

<400> 134

Met Phe Val Asn Gln Arg Thr Arg Arg Pro Tyr Met Ser Val Phe Val
1 5 10 15

Leu Val Leu Gly Ala Ala Val Ile Cys Pro Ala Tyr Gly Ile Ile Asp
20 25 30

Arg Leu Val Val Gln Thr Ser Ser Gly Pro Ile Arg Gly Arg Ser Thr
35 40 45

Met Val Gln Gly Arg Glu Val His Val Phe Asn Gly Val Pro Phe Ala
50 55 60

Lys Pro Pro Val Asp Ser Leu Arg Phe Lys Lys Pro Val Pro Ala Glu
65 70 75 80

Pro Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro Pro Ser Cys Ile
85 90 95

Gln Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ala Gly Glu Glu Met Trp
100 105 110

Asn Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Tyr Leu Asn Ile Trp
115 120 125

263365us-seq-list-082310 (2).txt

Val Pro Thr Lys Thr Arg Leu Arg His Gly Arg Gly Leu Asn Phe Gly
130 135 140

Ser Asn Asp Tyr Phe Gln Asp Asp Asp Asp Phe Gln Arg Gln His Gln
145 150 155 160

Ser Lys Gly Gly Leu Ala Met Leu Val Trp Ile Tyr Gly Gly Gly Phe
165 170 175

Met Ser Gly Thr Ser Thr Leu Asp Ile Tyr Asn Ala Glu Ile Leu Ala
180 185 190

Ala Val Gly Asn Val Ile Val Ala Ser Met Gln Tyr Arg Val Gly Ala
195 200 205

Phe Gly Phe Leu Tyr Leu Ala Pro Tyr Ile Asn Gly Tyr Glu Glu Asp
210 215 220

Ala Pro Gly Asn Met Gly Met Trp Asp Gln Ala Leu Ala Ile Arg Trp
225 230 235 240

Leu Lys Glu Asn Ala Lys Ala Phe Gly Gly Asp Pro Asp Leu Ile Thr
245 250 255

Leu Phe Gly Glu Ser Ala Gly Gly Ser Ser Val Ser Leu His Leu Leu
260 265 270

Ser Pro Val Thr Arg Gly Leu Ser Lys Arg Gly Ile Leu Gln Ser Gly
275 280 285

Thr Leu Asn Ala Pro Trp Ser His Met Thr Ala Glu Lys Ala Leu Gln
290 295 300

Ile Ala Glu Gly Leu Ile Asp Asp Cys Asn Cys Asn Leu Thr Met Leu
305 310 315 320

Lys Glu Ser Pro Ser Thr Val Met Gln Cys Met Arg Asn Val Asp Ala
325 330 335

Lys Thr Ile Ser Val Gln Gln Trp Asn Ser Tyr Ser Gly Ile Leu Gly
340 345 350

Phe Pro Ser Ala Pro Thr Ile Asp Gly Val Phe Met Thr Ala Asp Pro
355 360 365

Met Thr Met Leu Arg Glu Ala Asn Leu Glu Gly Ile Asp Ile Leu Val
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Gly Ser Asn Arg Asp Glu Gly Thr Tyr Phe Leu Leu Tyr Asp Phe Ile
385 390 395 400

Asp Tyr Phe Glu Lys Asp Ala Ala Thr Ser Leu Pro Arg Asp Lys Phe
405 410 415

Leu Glu Ile Met Asn Thr Ile Phe Asn Lys Ala Ser Glu Pro Glu Arg
420 425 430

Glu Ala Ile Ile Phe Gln Tyr Thr Gly Trp Glu Ser Gly Asn Asp Gly
435 440 445

Tyr Gln Asn Gln His Gln Val Gly Arg Ala Val Gly Asp His Phe Phe
450 455 460

Ile Cys Pro Thr Asn Glu Phe Ala Leu Gly Leu Thr Glu Arg Gly Ala
465 470 475 480

Ser Val His Tyr Tyr Tyr Phe Thr His Arg Thr Ser Thr Ser Leu Trp
485 490 495

Gly Glu Trp Met Gly Val Leu His Gly Asp Glu Val Glu Tyr Ile Phe
500 505 510

Gly Gln Pro Met Asn Ala Ser Leu Gln Tyr Arg Gln Arg Glu Arg Asp
515 520 525

Leu Ser Arg Arg Met Val Leu Ser Val Ser Glu Phe Ala Arg Thr Gly
530 535 540

Asn Pro Ala Leu Glu Gly Glu His Trp Pro Leu Tyr Thr Arg Glu Asn
545 550 555 560

Pro Ile Phe Phe Ile Phe Asn Ala Glu Gly Glu Asp Asp Leu Arg Gly
565 570 575

Glu Lys Tyr Gly Arg Gly Pro Met Ala Thr Ser Cys Ala Phe Trp Asn
580 585 590

Asp Phe Leu Pro Arg Leu Arg Ala Trp Ser Val Pro Ser Lys Ser Pro
595 600 605

Cys Asn Leu Leu Glu Gln Met Ser Ile Ala Ser Val Ser Ser Thr Met
610 615 620

Pro Ile Val Val Met Val Val Leu Val Leu Ile Pro Leu Cys Ala Trp
625 630 635 640

Trp Trp Ala Ile Lys Lys Asn Lys Thr Pro Pro His Pro Gln Val Ile
645 650 655

Leu Glu Thr Arg Ala Phe Met His
660

<210> 135

<211> 637

<212> PRT

<213> Aedes aegypti

<400> 135

Met Lys Met Ser Ala Val Val Arg Leu Cys Cys Asn Met Ile Ser Leu
1 5 10 15

Leu Leu Cys Ile Thr Val Ile Ser Pro Val Tyr Gly Ile Phe Asp Arg
20 25 30

Leu Val Val Gln Thr Ser Ser Gly Pro Ile Arg Gly Arg Ser Thr Met
35 40 45

Val Leu Gly Arg Glu Val His Val Phe Asn Gly Val Pro Phe Ala Lys
50 55 60

Pro Pro Val Asp Gly Leu Arg Phe Arg Lys Pro Val Pro Ala Glu Pro
65 70 75 80

Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro Pro Ser Cys Ile Gln
85 90 95

Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ala Gly Glu Glu Met Trp Asn
100 105 110

Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val
115 120 125

Pro Thr Lys Thr Arg Leu Arg His Gly Arg Gly Leu Asn Phe Gly Asn
130 135 140

Asn Asp Tyr Phe Gln Asp Asp Asp Asp Phe Gln Arg Gln His Gln Ser
145 150 155 160

Lys Gly Gly Leu Ala Met Leu Val Trp Ile Tyr Gly Gly Gly Phe Met
165 170 175

Ser Gly Thr Ser Thr Leu Asp Val Tyr Asn Ala Glu Met Leu Ala Ala
 180 185 190
 Val Gly Asn Val Ile Val Ala Ser Met Gln Tyr Arg Val Gly Ser Phe
 195 200 205
 Gly Phe Phe Tyr Leu Ala Pro Tyr Leu Asn Asp Asp Asp Ala Pro Gly
 210 215 220
 Asn Val Gly Leu Trp Asp Gln Ala Leu Ala Ile Arg Trp Leu Lys Glu
 225 230 235 240
 Asn Ala Lys Ala Phe Gly Gly Asp Pro Asp Leu Ile Thr Leu Phe Gly
 245 250 255
 Glu Ser Ala Gly Gly Ser Ser Val Ser Leu His Leu Leu Ser Pro Val
 260 265 270
 Thr Arg Gly Leu Ser Arg Arg Gly Ile Leu Gln Ser Gly Thr Leu Asn
 275 280 285
 Ala Pro Trp Ser His Met Ser Ala Glu Lys Ala Leu Ser Val Ala Glu
 290 295 300
 Ala Leu Ile Asp Asp Cys Asn Cys Asn Val Thr Leu Leu Lys Asp Asn
 305 310 315 320
 Pro Asn Tyr Val Met Asn Cys Met Arg Asn Val Asp Ala Lys Thr Ile
 325 330 335
 Ser Val Gln Gln Trp Asn Ser Tyr Ser Gly Ile Leu Gly Phe Pro Ser
 340 345 350
 Ala Pro Thr Ile Asp Gly Val Phe Met Thr Ala Asp Pro Met Thr Met
 355 360 365
 Leu Arg Glu Ala Asn Leu Glu Gly Val Glu Ile Leu Val Gly Ser Asn
 370 375 380
 Arg Asp Glu Gly Thr Tyr Phe Leu Leu Tyr Asp Phe Ile Asp Tyr Phe
 385 390 395 400
 Glu Lys Asp Ala Ala Thr Ser Leu Pro Arg Asp Lys Phe Leu Glu Ile
 405 410 415
 Met Asn Thr Ile Phe Ser Lys Ala Ser Glu Pro Glu Arg Glu Ala Ile
 420 425 430

263365us-seq-list-082310 (2).txt

Ile Phe Gln Tyr Thr Gly Trp Glu Ser Gly Asn Asp Gly Tyr Gln Asn
435 440 445

Gln Gln Gln Val Gly Arg Ser Val Gly Asp His Phe Phe Ile Cys Pro
450 455 460

Thr Asn Glu Phe Ala Leu Gly Leu Ala Glu Arg Gly Ala Ser Val Tyr
465 470 475 480

Tyr Tyr Tyr Phe Thr His Arg Thr Ser Thr Ser Leu Trp Gly Glu Trp
485 490 495

Met Gly Val Leu His Gly Asp Glu Val Glu Tyr Ile Phe Gly Gln Pro
500 505 510

Met Asn Val Ser Met Gln Tyr Arg Gln Arg Glu Arg Asp Leu Ser Arg
515 520 525

Arg Met Val Leu Ser Val Ser Glu Phe Ala Arg Ser Gly Asn Pro Ala
530 535 540

Leu Glu Gly Glu His Trp Pro Val Tyr Thr Lys Glu Asn Pro Ile Tyr
545 550 555 560

Phe Ile Phe Asn Ala Glu Gly Glu Asp Asp Leu Arg Gly Glu Lys Tyr
565 570 575

Gly Arg Gly Pro Met Ala Thr Ala Cys Ala Phe Trp Asn Asp Phe Leu
580 585 590

Pro Arg Leu Arg Ala Trp Ser Val Pro Pro Lys Ser Ser Cys Asn Ile
595 600 605

Leu Glu Gln Thr Ser Ala Ala Thr Ile Leu Tyr Val Asp Ile Lys Ile
610 615 620

Val Thr Val Leu Met Val Phe Ile Leu Val Arg Leu Tyr
625 630 635

<210> 136
<211> 649
<212> PRT
<213> Drosophila melanogaster
<400> 136

Met Ala Ile Ser Cys Arg Gln Ser Arg Val Leu Pro Met Ser Leu Pro
1 5 10 15

263365us-seq-list-082310 (2).txt

Leu Pro Leu Thr Ile Pro Leu Pro Leu Val Leu Val Leu Ser Leu His
 20 25 30
 Leu Ser Gly Val Cys Gly Val Ile Asp Arg Leu Val Val Gln Thr Ser
 35 40 45
 Ser Gly Pro Val Arg Gly Arg Ser Val Thr Val Gln Gly Arg Glu Val
 50 55 60
 His Val Tyr Thr Gly Ile Pro Tyr Ala Lys Pro Pro Val Glu Asp Leu
 65 70 75 80
 Arg Phe Arg Lys Pro Val Pro Ala Glu Pro Trp His Gly Val Leu Asp
 85 90 95
 Ala Thr Arg Leu Ser Ala Thr Cys Val Gln Glu Arg Tyr Glu Tyr Phe
 100 105 110
 Pro Gly Phe Ser Gly Glu Glu Ile Trp Asn Pro Asn Thr Asn Val Ser
 115 120 125
 Glu Asp Cys Leu Tyr Ile Asn Val Trp Ala Pro Ala Lys Ala Arg Leu
 130 135 140
 Arg His Gly Arg Gly Ala Asn Gly Gly Glu His Pro Asn Gly Lys Gln
 145 150 155 160
 Ala Asp Thr Asp His Leu Ile His Asn Gly Asn Pro Gln Asn Thr Thr
 165 170 175
 Asn Gly Leu Pro Ile Leu Ile Trp Ile Tyr Gly Gly Gly Phe Met Thr
 180 185 190
 Gly Ser Ala Thr Leu Asp Ile Tyr Asn Ala Asp Ile Met Ala Ala Val
 195 200 205
 Gly Asn Val Ile Val Ala Ser Phe Gln Tyr Arg Val Gly Ala Phe Gly
 210 215 220
 Phe Leu His Leu Ala Pro Glu Met Pro Ser Glu Phe Ala Glu Glu Ala
 225 230 235 240
 Pro Gly Asn Val Gly Leu Trp Asp Gln Ala Leu Ala Ile Arg Trp Leu
 245 250 255
 Lys Asp Asn Ala His Ala Phe Gly Gly Asn Pro Glu Trp Met Thr Leu
 260 265 270

263365us-seq-list-082310 (2).txt

Phe Gly Glu Ser Ala Gly Ser Ser Ser Val Asn Ala Gln Leu Met Ser
275 280 285

Pro Val Thr Arg Gly Leu Val Lys Arg Gly Met Met Gln Ser Gly Thr
290 295 300

Met Asn Ala Pro Trp Ser His Met Thr Ser Glu Lys Ala Val Glu Ile
305 310 315 320

Gly Lys Ala Leu Ile Asn Asp Cys Asn Cys Asn Ala Ser Met Leu Lys
325 330 335

Thr Asn Pro Ala His Val Met Ser Cys Met Arg Ser Val Asp Ala Lys
340 345 350

Thr Ile Ser Val Gln Gln Trp Asn Ser Tyr Ser Gly Ile Leu Ser Phe
355 360 365

Pro Ser Ala Pro Thr Ile Asp Gly Ala Phe Leu Pro Ala Asp Pro Met
370 375 380

Thr Leu Met Lys Thr Ala Asp Leu Lys Asp Tyr Asp Ile Leu Met Gly
385 390 395 400

Asn Val Arg Asp Glu Gly Thr Tyr Phe Leu Leu Tyr Asp Phe Ile Asp
405 410 415

Tyr Phe Asp Lys Asp Asp Ala Thr Ala Leu Pro Arg Asp Lys Tyr Leu
420 425 430

Glu Ile Met Asn Asn Ile Phe Gly Lys Ala Thr Gln Ala Glu Arg Glu
435 440 445

Ala Ile Ile Phe Gln Tyr Thr Ser Trp Glu Gly Asn Pro Gly Tyr Gln
450 455 460

Asn Gln Gln Gln Ile Gly Arg Ala Val Gly Asp His Phe Phe Thr Cys
465 470 475 480

Pro Thr Asn Glu Tyr Ala Gln Ala Leu Ala Glu Arg Gly Ala Ser Val
485 490 495

His Tyr Tyr Tyr Phe Thr His Arg Thr Ser Thr Ser Leu Trp Gly Glu
500 505 510

Trp Met Gly Val Leu His Gly Asp Glu Ile Glu Tyr Phe Phe Gly Gln
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Pro Leu Asn Asn Ser Leu Gln Tyr Arg Pro Val Glu Arg Glu Leu Gly
530 535 540

Lys Arg Met Leu Ser Ala Val Ile Glu Phe Ala Lys Thr Gly Asn Pro
545 550 555 560

Ala Gln Asp Gly Glu Glu Trp Pro Asn Phe Ser Lys Glu Asp Pro Val
565 570 575

Tyr Tyr Ile Phe Ser Thr Asp Asp Lys Ile Glu Lys Leu Ala Arg Gly
580 585 590

Pro Leu Ala Ala Arg Cys Ser Phe Trp Asn Asp Tyr Leu Pro Lys Val
595 600 605

Arg Ser Trp Ala Gly Thr Cys Asp Gly Asp Ser Gly Ser Ala Ser Ile
610 615 620

Ser Pro Arg Leu Gln Leu Leu Gly Ile Ala Ala Leu Ile Tyr Ile Cys
625 630 635 640

Ala Ala Leu Arg Thr Lys Arg Val Phe
645

<210> 137
<211> 708
<212> PRT
<213> Lucilia cuprina

<400> 137

Met Ala Arg Phe Ile Thr Thr Ser Ser Ser Pro Thr Leu Thr Thr Ser
1 5 10 15

Thr Ala Ala Thr Ala Pro Ser Ser Ser Trp Ser Ser Asn Ala Thr Ser
20 25 30

Thr Ala Thr Ser Ile Ser Ser His Ser Arg Thr Ser Arg Lys Ser Arg
35 40 45

Tyr Thr Ser Ser Asn Leu Leu Asn Ala Phe Ala Ser Leu Thr Ser Arg
50 55 60

Ser Ser Leu Ser Leu Ser Ser Thr Ser Ser Asn Asp Leu Tyr Arg Gly
65 70 75 80

Phe Leu Thr Thr Leu Val Ile Leu Leu Arg Met Ser Ser Val Ala Tyr
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Gly Ile Thr Asp Arg Leu Ile Val Gln Thr Thr Ser Gly Pro Val Arg
100 105 110

Gly Arg Ala Val Thr Val Gln Gly Arg Glu Val His Val Phe Thr Gly
115 120 125

Ile Pro Tyr Ala Lys Pro Pro Val Asp Asp Leu Arg Phe Arg Lys Pro
130 135 140

Val Pro Ala Glu Pro Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro
145 150 155 160

Ala Thr Cys Val Gln Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ser Gly
165 170 175

Glu Glu Ile Trp Asn Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Tyr
180 185 190

Met Asn Ile Trp Ala Pro Ala Lys Ala Arg Leu Arg His Gly Arg Gly
195 200 205

Ala Asn Gly Gly Glu His Ser Ser Lys Thr Asp Pro Asp His Leu Ile
210 215 220

His Ser Ala Thr Pro Gln Asn Thr Thr Asn Gly Leu Pro Ile Leu Ile
225 230 235 240

Trp Ile Tyr Gly Gly Gly Phe Met Thr Gly Ser Ala Thr Leu Asp Ile
245 250 255

Tyr Asn Ala Asp Ile Met Ser Ala Val Gly Asn Val Ile Val Ala Ser
260 265 270

Phe Gln Tyr Arg Val Gly Ala Phe Gly Phe Leu His Leu Ser Pro Val
275 280 285

Met Pro Gly Phe Glu Glu Glu Ala Pro Gly Asn Val Gly Leu Trp Asp
290 295 300

Gln Ala Leu Ala Leu Arg Trp Leu Lys Glu Asn Ala Arg Ala Phe Gly
305 310 315 320

Gly Asn Pro Glu Trp Met Thr Leu Phe Gly Glu Ser Ala Gly Ser Ser
325 330 335

Ser Val Asn Ala Gln Leu Val Ser Pro Val Thr Arg Gly Leu Val Lys
 340 345 350

Arg Gly Met Met Gln Ser Gly Thr Met Asn Ala Pro Trp Ser His Met
 355 360 365

Thr Ser Glu Lys Ala Val Glu Ile Gly Lys Ala Leu Ile Asn Asp Cys
 370 375 380

Asn Cys Asn Ala Ser Leu Leu Pro Ala Asn Pro Gln Ser Val Met Ala
 385 390 395 400

Cys Met Arg Ala Val Asp Ala Lys Thr Ile Ser Val Gln Gln Trp Asn
 405 410 415

Ser Tyr Ser Gly Ile Leu Ser Phe Pro Ser Ala Pro Thr Ile Asp Gly
 420 425 430

Ala Phe Leu Pro Ala Asp Pro Met Thr Leu Met Lys Thr Ala Asp Met
 435 440 445

Ser Gly Tyr Asp Ile Met Ile Gly Asn Val Lys Asp Glu Gly Thr Tyr
 450 455 460

Phe Leu Leu Tyr Asp Phe Ile Asp Tyr Phe Asp Lys Asp Glu Ala Thr
 465 470 475 480

Ser Leu Pro Arg Asp Lys Tyr Leu Glu Ile Met Asn Asn Ile Phe Asn
 485 490 495

Lys Ala Thr Gln Ala Glu Arg Glu Ala Ile Ile Phe Gln Tyr Thr Ser
 500 505 510

Trp Glu Gly Asn Pro Gly Tyr Gln Asn Gln Gln Gln Ile Gly Arg Ala
 515 520 525

Val Gly Asp His Phe Phe Thr Cys Pro Thr Asn Glu Tyr Ala Gln Ala
 530 535 540

Leu Ala Glu Arg Gly Ala Gln Val His Tyr Tyr Tyr Phe Thr His Arg
 545 550 555 560

Thr Ser Thr Ser Leu Trp Gly Glu Trp Met Gly Val Leu His Gly Asp
 565 570 575

Glu Ile Glu Tyr Phe Phe Gly Gln Pro Leu Asn Thr Ser Leu Gln Tyr
 580 585 590

263365us-seq-list-082310 (2).txt

Arg Ala Val Glu Arg Glu Leu Gly Lys Arg Met Leu Asn Ser Val Ile
595 600 605

Glu Phe Ala Lys Thr Gly Asn Pro Ala Val Asp Gly Glu Glu Trp Pro
610 615 620

Asn Phe Ser Lys Glu Asp Pro Val Tyr Tyr Val Phe Ser Thr Asp Glu
625 630 635 640

Lys Thr Glu Lys Leu Gln Arg Gly Pro Leu Ala Lys Arg Cys Ser Phe
645 650 655

Trp Asn Asp Tyr Leu Pro Lys Val Arg Ser Trp Val Gly Ser Glu Cys
660 665 670

Glu Asn Asn Ser Ala Glu Ser Ala Ala Val Ser Ile Ile Tyr Glu Lys
675 680 685

Gln Gln Asn Leu Leu Lys Trp Val Ile Met Leu Thr Ile Met Val Thr
690 695 700

Cys Ile Phe Gln
705

<210> 138
<211> 692
<212> PRT
<213> Musca domestica

<400> 138

Met Ala Arg Ser Val Arg Thr Pro Ile Ser Pro Ser Ser Ser Ser Ser
1 5 10 15

Ser Ser Arg Ser Ser Trp Ser Ser Pro Ser Ser Ser Phe Tyr Ser Leu
20 25 30

Leu Ser Ser Phe Lys Ala Ser Leu Thr Arg Pro Ser Ser Ser Ser Ser
35 40 45

Val Ala His His Leu Ala Ala Arg Asn Asn Asp Ile Cys Arg Gly Leu
50 55 60

Phe Ala Thr Leu Val Ile Leu Leu Arg Met Ser Ala Leu Thr Ser Ala
65 70 75 80

Met Thr Asp His Leu Thr Val Gln Thr Thr Ser Gly Pro Val Arg Gly
85 90 95

263365us-seq-list-082310 (2).txt

Arg Ser Val Thr Val Gln Gly Arg Asp Val His Val Phe Thr Gly Ile
100 105 110

Pro Tyr Ala Lys Pro Pro Val Asp Asp Leu Arg Phe Arg Lys Pro Val
115 120 125

Pro Ala Glu Pro Trp His Gly Val Leu Asp Ala Thr Arg Leu Pro Ala
130 135 140

Thr Cys Val Gln Glu Arg Tyr Glu Tyr Phe Pro Gly Phe Ser Gly Glu
145 150 155 160

Glu Ile Trp Asn Pro Asn Thr Asn Val Ser Glu Asp Cys Leu Phe Met
165 170 175

Asn Ile Trp Ala Pro Ala Lys Ala Arg Leu Arg His Gly Arg Gly Thr
180 185 190

Asn Gly Gly Glu His Ser Ser Lys Thr Asp Gln Asp His Leu Ile His
195 200 205

Ser Ala Thr Pro Gln Asn Thr Thr Asn Gly Leu Pro Ile Leu Ile Trp
210 215 220

Ile Tyr Gly Gly Gly Phe Met Thr Gly Ser Ala Thr Leu Asp Ile Tyr
225 230 235 240

Asn Ala Glu Ile Met Ser Ala Val Gly Asn Val Ile Val Ala Ser Phe
245 250 255

Gln Tyr Arg Val Gly Ala Phe Gly Phe Leu His Leu Ser Pro Val Met
260 265 270

Pro Gly Phe Glu Glu Glu Ala Pro Gly Asn Val Gly Leu Trp Asp Gln
275 280 285

Ala Leu Ala Leu Arg Trp Leu Lys Glu Asn Ala Arg Ala Phe Gly Gly
290 295 300

Asn Pro Glu Trp Met Thr Leu Phe Gly Glu Ser Ala Gly Ser Ser Ser
305 310 315 320

Val Asn Ala Gln Leu Met Ser Pro Val Thr Arg Gly Leu Val Lys Arg
325 330 335

Gly Met Met Gln Ser Gly Thr Met Asn Ala Pro Trp Ser His Met Thr
340 345 350

263365us-seq-list-082310 (2).txt

Ser Glu Lys Ala Val Glu Ile Gly Lys Ala Leu Val Asn Asp Cys Asn
355 360 365

Cys Asn Ala Ser Leu Leu Pro Glu Asn Pro Gln Ala Val Met Ala Cys
370 375 380

Met Arg Gln Val Asp Ala Lys Thr Ile Ser Val Gln Gln Trp Asn Ser
385 390 395 400

Tyr Ser Gly Ile Leu Ser Phe Pro Ser Ala Pro Thr Ile Asp Gly Ala
405 410 415

Phe Leu Pro Ala Asp Pro Met Thr Leu Leu Lys Thr Ala Asp Leu Ser
420 425 430

Gly Tyr Asp Ile Leu Ile Gly Asn Val Lys Asp Glu Gly Thr Tyr Phe
435 440 445

Leu Leu Tyr Asp Phe Ile Asp Tyr Phe Asp Lys Asp Asp Ala Thr Ser
450 455 460

Leu Pro Arg Asp Lys Tyr Leu Glu Ile Met Asn Asn Ile Phe Gln Lys
465 470 475 480

Ala Ser Gln Ala Glu Arg Glu Ala Ile Ile Phe Gln Tyr Thr Ser Trp
485 490 495

Glu Gly Asn Pro Gly Tyr Gln Asn Gln Gln Gln Ile Gly Arg Ala Val
500 505 510

Gly Asp His Phe Phe Thr Cys Pro Thr Asn Glu Tyr Ala Gln Ala Leu
515 520 525

Ala Glu Arg Gly Ala Ser Val His Tyr Tyr Tyr Phe Thr His Arg Thr
530 535 540

Ser Thr Ser Leu Trp Gly Glu Trp Met Gly Val Leu His Gly Asp Glu
545 550 555 560

Ile Glu Tyr Phe Phe Gly Gln Pro Leu Asn Asn Ser Leu Gln Tyr Arg
565 570 575

Pro Val Glu Arg Glu Leu Gly Lys Arg Met Leu Asn Ser Val Ile Glu
580 585 590

Phe Ala Lys Ser Gly Asn Pro Ala Val Asp Gly Glu Glu Trp Pro Asn
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595

Phe Ser Lys Glu Asp Pro Val Tyr Tyr Val Phe Ser Thr Asp Glu Lys
610 615 620

Ile Glu Lys Leu Gln Arg Gly Pro Leu Ala Lys Arg Cys Ser Phe Trp
625 630 635 640

Asn Asp Tyr Leu Pro Lys Val Arg Ser Trp Ile Gly Ser Glu Cys Glu
645 650 655

Asn Lys Ser Ser Thr Ser Ala Ser Ala Ala Ile Tyr Glu Met Lys Met
660 665 670

Gln Gln Leu Thr Leu Leu Ala Val Ala Ile Ile Leu Thr Met Val Asn
675 680 685

Ser Ile Phe Gln
690

<210> 139
<211> 635
<212> PRT
<213> Culex pipiens

<400> 139

Met Ser Ser Ile Ser Met Val Val Gly Ala Val Leu Leu Leu Cys Ser
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Ala Val Ile Ser Pro Val Tyr Gly Ala Phe Asp Arg Leu Val Val Arg
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Thr Ser Ser Gly Pro Ile Arg Gly Arg Ser Thr Met Val Gln Gly Arg
35 40 45

Glu Val His Val Phe Asn Gly Val Pro Phe Ala Lys Pro Pro Val Asp
50 55 60

Gly Leu Arg Phe Gln Lys Pro Val Pro Ala Glu Pro Trp His Gly Val
65 70 75 80

Leu Asp Ala Thr Arg Leu Pro Pro Ser Cys Ile Gln Glu Arg Tyr Glu
85 90 95

Tyr Phe Pro Gly Phe Ala Gly Glu Glu Met Trp Asn Pro Asn Thr Asn
100 105 110

Val Ser Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Thr Lys Thr
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Arg Leu Arg His Gly Arg Gly Leu Asn Phe Gly Asn Asn Asp Tyr Phe
130 135 140

Gln Asp Asp Glu Asp Phe Gln Arg Gln His Gln Ser Lys Gly Gly Leu
145 150 155 160

Ala Met Leu Val Trp Ile Cys Gly Gly Gly Phe Met Ser Gly Thr Ser
165 170 175

Thr Leu Asp Val Tyr Asn Ala Glu Ile Leu Ala Ala Val Gly Asn Val
180 185 190

Ile Val Ala Ser Met Gln Tyr Arg Val Gly Ala Phe Gly Phe Phe Tyr
195 200 205

Leu Ser Pro Tyr Leu Asn Gly Arg Glu Glu Glu Ala Pro Gly Asn Val
210 215 220

Gly Leu Trp Asp Gln Ala Leu Ala Ile Arg Trp Leu Lys Glu Asn Ala
225 230 235 240

Lys Ala Phe Gly Gly Asp Pro Asp Leu Ile Thr Leu Phe Gly Glu Ser
245 250 255

Ala Gly Gly Ser Ser Val Ser Leu His Leu Leu Ser Pro Ala Thr Arg
260 265 270

Gly Leu Ser His Arg Gly Ile Leu Gln Ser Gly Thr Leu Asn Ala Pro
275 280 285

Trp Ser His Met Thr Ala Glu Lys Ala Leu Ser Val Ala Glu Ser Leu
290 295 300

Ile Asp Asp Cys Asn Cys Asn Val Thr Leu Leu Lys Asp Ser Pro Ser
305 310 315 320

Ser Val Met His Cys Met Arg Asn Val Asp Ala Lys Thr Ile Ser Val
325 330 335

Gln Gln Trp Asn Ser Tyr Ser Gly Ile Leu Gly Phe Pro Ser Ala Pro
340 345 350

Thr Ile Asp Gly Val Phe Met Thr Ala Asp Pro Met Thr Met Leu Arg
355 360 365

Glu Ala Asn Leu Glu Gly Ile Asp Ile Leu Val Gly Ser Asn Arg Asp
370 375 380

Glu Gly Thr Tyr Phe Leu Leu Tyr Asp Phe Ile Asp Tyr Phe Glu Lys
385 390 395 400

Asp Ala Ala Thr Ser Leu Pro Arg Asp Lys Phe Leu Glu Ile Met Asn
405 410 415

Thr Ile Phe Ser Lys Ala Ser Glu Pro Glu Arg Glu Ala Ile Ile Phe
420 425 430

Gln Tyr Thr Gly Trp Glu Ser Gly Asn Asp Gly Tyr Gln Asn Gln Gln
435 440 445

Gln Val Gly Arg Ala Val Gly Asp His Phe Phe Ile Cys Pro Thr Asn
450 455 460

Glu Phe Ala Leu Gly Leu Thr Glu Gln Gly Ala Ser Val His Tyr Tyr
465 470 475 480

Tyr Phe Thr His Arg Thr Ser Thr Ser Leu Trp Gly Glu Trp Met Gly
485 490 495

Val Leu His Gly Asp Glu Val Glu Tyr Ile Phe Gly Gln Pro Met Asn
500 505 510

Ala Thr Leu Gln Tyr Arg Gln Arg Glu Arg Asp Leu Ser Arg Arg Met
515 520 525

Val Leu Ser Val Ser Glu Phe Ala Arg Ser Gly Asn Pro Ala Leu Glu
530 535 540

Gly Glu His Trp Pro Leu Tyr Thr Lys Glu Asn Pro Ile Tyr Phe Ile
545 550 555 560

Phe Asn Ala Glu Gly Glu Asp Asp Leu Arg Gly Glu Lys Tyr Gly Arg
565 570 575

Gly Pro Met Ala Thr Ser Cys Ala Phe Trp Asn Asp Phe Leu Pro Arg
580 585 590

Leu Arg Ala Trp Ser Ile Pro Pro Lys Ser Ser Cys Asn Leu Leu Glu
595 600 605

Pro Thr Ser Gly Ala Pro Val Arg Tyr Val Asp Ile Lys Val Leu Thr
610 615 620

263365us-seq-list-082310 (2).txt

Val Leu Thr Val Leu Ile Val Leu Arg Leu Phe
625 630 635

<210> 140
<211> 91
<212> PRT
<213> Anopheles gambiae

<400> 140

Thr Glu Pro Asp Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met
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Val Gly Asp Tyr His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg
20 25 30

Tyr Ala Glu Glu Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg
35 40 45

Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
50 55 60

Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
65 70 75 80

Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
85 90

<210> 141
<211> 2109
<212> DNA
<213> Culex pipiens

<400> 141
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gcatttttta caccatatat aggtcacgga gattctgttc gaattgtaga tgccgaatta 300
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agatggaccg gtgtgctgaa cgcgaccaa cgcaccaact cctgcgtcca gatcgtggac 600
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263365us-seq-list-082310 (2).txt

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cggacgctgg cctcggagga gaacgtgatc gtagtttcgc tgcagtaccg tgtcgcaagt 840
cttgggtttc tcttcctcgg cacaccggag gcacccggta acgcggggct gtttgatcag 900
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aagatttaa 2109

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<210> 142
 <211> 623
 <212> PRT
 <213> Anopheles gambiae

<400> 142

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 20 25 30

Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala Asn Asp
 35 40 45

Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile
 50 55 60

Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile
 65 70 75 80

Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg
 85 90 95

Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn
 100 105 110

Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
 115 120 125

Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
 130 135 140

Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
 145 150 155 160

Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
 165 170 175

Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
 180 185 190

Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro
 195 200 205

Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg
 210 215 220

Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val
 225 230 235 240

Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu
 245 250 255

Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser
 260 265 270

263365us-seq-list-082310 (2).txt

Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr
275 280 285

Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro
290 295 300

Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His
305 310 315 320

Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro
325 330 335

Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg
340 345 350

Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser
355 360 365

Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu
370 375 380

Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln
385 390 395 400

Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala
405 410 415

Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser
420 425 430

Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys
435 440 445

Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val
450 455 460

Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg
465 470 475 480

Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu
485 490 495

Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser
500 505 510

Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro
515 520 525

263365us-seq-list-082310 (2).txt

Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr
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Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val
545 550 555 560

Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr Leu
565 570 575

Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala Pro Pro
580 585 590

Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp Leu Ile
595 600 605

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610 615 620

<210> 143
<211> 2534
<212> DNA
<213> Anopheles gambiae

<400> 143
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263365us-seq-list-082310 (2).txt

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<210> 144
<211> 623
<212> PRT
<213> Anopheles gambiae
<400> 144

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263365us-seq-list-082310 (2).txt

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Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala Thr Pro
20 25 30

Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala Asn Asp
35 40 45

Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile
50 55 60

Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile
65 70 75 80

Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg
85 90 95

Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn
100 105 110

Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
115 120 125

Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
130 135 140

Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
145 150 155 160

Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
165 170 175

Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
180 185 190

Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro
195 200 205

Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg
210 215 220

Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val
225 230 235 240

Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu
245 250 255

263365us-seq-list-082310 (2).txt

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260 265 270

Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr
275 280 285

Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro
290 295 300

Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His
305 310 315 320

Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro
325 330 335

Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg
340 345 350

Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser
355 360 365

Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu
370 375 380

Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln
385 390 395 400

Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala
405 410 415

Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser
420 425 430

Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys
435 440 445

Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val
450 455 460

Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg
465 470 475 480

Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu
485 490 495

Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser
500 505 510

263365us-seq-list-082310 (2).txt

Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro
515 520 525

Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr
530 535 540

Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val
545 550 555 560

Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr Leu
565 570 575

Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala Pro Pro
580 585 590

Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp Leu Ile
595 600 605

Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg Phe Ile Gln
610 615 620

<210> 145
<211> 194
<212> DNA
<213> Anopheles gambiae

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gagaacgtga tcgt 194

<210> 146
<211> 194
<212> DNA
<213> Anopheles gambiae

<400> 146
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agcttctact ccggcaccgc caccctggac gtgtacgacc accgggcgct tgcgtcggag 180
gagaacgtga tcgt 194

<210> 147
<211> 194
<212> DNA

<213> *Culex pipiens*

<400> 147
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 ggcttctact ccgggactgc cacgctggac gtgtacgacc atcggacgct ggcctcggag 180
 gagaacgtga tcgt 194

<210> 148
 <211> 194
 <212> DNA
 <213> *Culex pipiens*

<400> 148
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 gtggtcgtgc caaggccgag gccaagaat gccgccgtca tgctgtggat ctttgggggt 120
 agcttctact ccgggactgc cacgttggac gtgtacgacc atcggacgct ggcctcggag 180
 gagaacgtga tcgt 194

<210> 149
 <211> 194
 <212> DNA
 <213> *Anopheles albimanus*

<400> 149
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 ggcttctact ccggtacggc cacactggac gtgtacgacc accgggagct cgcctcggaa 180
 gagaacgtta tcgt 194

<210> 150
 <211> 194
 <212> DNA
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